

## SEQUENCE LISTING

<110> Bryan, Bruce  
 Szent-Gyorgyi, Christopher  
 Szczepaniak, William

<120> RENILLA RENIFORMIS FLOURESCENT PROTEINS, NUCLEIC ACIDS ENCODING THE  
 FLOURESCENT PROTEINS AND THE USE THEREOF IN DIAGNOSTICS, HIGH THROUGHPUT  
 SCREENING AND NOVELTY ITEMS

<130> 24729-128

<140> Not Yet Assigned

<141> Herewith

<150> 60/189,691

<151> 2000-03-15

<150> 09/277,716

<151> 1999-03-26

<150> 08/757,046

<151> 1996-11-25

<150> 08/597,274

<151> 1996-02-06

<150> 08/908,909

<151> 1997-08-08

<150> 08/990,103

<151> 1997-12-12

<160> 33

<170> FastSEQ for Windows Version 4.0

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<211> 1196

<212> DNA

<213> Renilla reniformis

<220>

<221> CDS

<222> (1)...(942)

<223> Renilla reniformas luciferase

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gct gtt att ttt tta cat ggt aac gcg gcc tct tct tat tta tgg cga	192
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His Val Val Pro His Ile Glu Pro Val Ala Arg Cys Ile Ile Pro Asp	
65 70 75 80	
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Leu Ile Gly Met Gly Lys Ser Gly Lys Ser Gly Asn Gly Ser Tyr Arg	
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tta ctt gat cat tac aaa tat ctt act gca tgg ttg aac ttc tta att	336
Leu Leu Asp His Tyr Lys Tyr Leu Thr Ala Trp Leu Asn Phe Leu Ile	
100 105 110	
tac caa aga aga tca ttt ttt gtc ggc cat gat tgg ggt gct tgt ttg	384
Tyr Gln Arg Arg Ser Phe Phe Val Gly His Asp Trp Gly Ala Cys Leu	
115 120 125	
gca ttt cat tat agc tat gag cat caa gat aag atc aaa gca ata gtt	432
Ala Phe His Tyr Ser Tyr Glu His Gln Asp Lys Ile Lys Ala Ile Val	
130 135 140	
cac gct gaa agt gta gta gat gtg att gaa tca tgg gat gaa tgg cct	480
His Ala Glu Ser Val Val Asp Val Ile Glu Ser Trp Asp Glu Trp Pro	
145 150 155 160	
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Asp Ile Glu Glu Asp Ile Ala Leu Ile Lys Ser Glu Glu Gly Glu Lys	
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180 185 190	
atc atg aga aag tta gaa cca gaa gaa ttt gca gca tat ctt gaa cca	624
Ile Met Arg Lys Leu Glu Pro Glu Glu Phe Ala Ala Tyr Leu Glu Pro	
195 200 205	
ttc aaa gag aaa ggt gaa gtt cgt cgt cca aca tta tca tgg cct cgt	672
Phe Lys Glu Lys Gly Glu Val Arg Arg Pro Thr Leu Ser Trp Pro Arg	
210 215 220	
gaa atc ccg tta gta aaa ggt ggt aaa cct gac gtt gta caa att gtt	720
Glu Ile Pro Leu Val Lys Gly Gly Lys Pro Asp Val Val Gln Ile Val	
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260 265 270	
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Ala Lys Lys Phe Pro Asn Thr Glu Phe Val Lys Val Lys Gly Leu His	
275 280 285	
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atcattttgg aatattacct ctttcaatga aactttataa acagtgggtc aattaattaa 1142
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Asn Cys Gln Asp Ala Cys Pro Val Glu Ala Glu Ala Pro Ser Ser Thr
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cca aca gtc cca aca tct tgt gaa gct aaa gaa gga gaa tgt atc gat 144
Pro Thr Val Pro Thr Ser Cys Glu Ala Lys Glu Gly Glu Cys Ile Asp
35 40 45

acc aga tgc gca aca tgt aaa cga gac ata cta tca gac gga ctg tgt 192
Thr Arg Cys Ala Thr Cys Lys Arg Asp Ile Leu Ser Asp Gly Leu Cys
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65 70 75 80

gaa tcc aga gta gaa gct gct gga tat ttt aga acg ttt tac gcc aaa 288
Glu Ser Arg Val Glu Ala Ala Gly Tyr Phe Arg Thr Phe Tyr Ala Lys
85 90 95

aga ttt aat ttt cag gaa cct ggt aaa tat gtg ctg gct cga gga acc 336
Arg Phe Asn Phe Gln Glu Pro Gly Lys Tyr Val Leu Ala Arg Gly Thr
100 105 110

aag ggt ggc gac tgg tct gta acc ctc acc atg gag aat cta gat gga 384
Lys Gly Gly Asp Trp Ser Val Thr Leu Thr Met Glu Asn Leu Asp Gly
115 120 125

cag aag gga gct gta ctg act aag aca aca ctg gag gta gta gga gac 432
Gln Lys Gly Ala Val Leu Thr Lys Thr Thr Leu Glu Val Val Gly Asp
130 135 140

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Val Ile Asp Ile Thr Gln Ala Thr Ala Asp Pro Ile Thr Val Asn Gly
145 150 155 160

gga gct gac cca gtt atc gct aac ccg ttc aca att ggt gag gtg acc 528
Gly Ala Asp Pro Val Ile Ala Asn Pro Phe Thr Ile Gly Glu Val Thr
165 170 175

att gct gtt gtc gaa ata ccc ggc ttc aat att aca gtc atc gaa ttc 576
Ile Ala Val Val Glu Ile Pro Gly Phe Asn Ile Thr Val Ile Glu Phe
180 185 190

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ttt aaa cta atc gtg ata gat att ctg gga gga aga tct gtg aga att Phe Lys Leu Ile Val Ile Asp Ile Leu Gly Gly Arg Ser Val Arg Ile 195 200 205	624
gct cca gac aca gca aac aaa gga ctg ata tct ggt atc tgt ggt aat Ala Pro Asp Thr Ala Asn Lys Gly Leu Ile Ser Gly Ile Cys Gly Asn 210 215 220	672
ctg gag atg aat gac gct gat gac ttt act aca gac gca gat cag ctg Leu Glu Met Asn Asp Ala Asp Asp Phe Thr Thr Asp Ala Asp Gln Leu 225 230 235 240	720
gcg atc caa ccc aac ata aac aaa gag ttc gac ggc tgc cca ttc tac Ala Ile Gln Pro Asn Ile Asn Lys Glu Phe Asp Gly Cys Pro Phe Tyr 245 250 255	768
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Phe	Phe	Asp	Ala	Glu	Gly	Ala	Cys	Ala	Leu	Thr	Pro	Asn	Pro	Pro	Gly		
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Phe	Cys	Asp	His	Ala	Trp	Glu	Phe	Lys	Lys	Glu	Cys	Tyr	Ile	Lys	His		
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Phe	Tyr	Pro	Ile	Glu	Glu	Gly	Ser	Ala	Gly	Thr	Gln	Leu	Arg	Lys	Tyr		
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 Pro Leu Phe Lys Ala Lys Val Ile Asp Leu Asp Thr Lys Lys Ser Leu  
 370 375 380  
 ggt cct aac aga cgt gga gaa gtt tgt gtt aaa gga cct atg ctt atg 1200  
 Gly Pro Asn Arg Arg Gly Glu Val Cys Val Lys Gly Pro Met Leu Met  
 385 390 395 400  
 aaa ggt tat gta aat aat cca gaa gca aca aaa gaa ctt att gac gaa 1248  
 Lys Gly Tyr Val Asn Asn Pro Glu Ala Thr Lys Glu Leu Ile Asp Glu  
 405 410 415  
 gaa ggt tgg ctg cac acc gga gat att gga tat tat gat gaa gaa aaa 1296  
 Glu Gly Trp Leu His Thr Gly Asp Ile Gly Tyr Tyr Asp Glu Glu Lys  
 420 425 430  
 cat ttc ttt att gtc gat cgt ttg aag tct tta atc aaa tac aaa gga 1344  
 His Phe Phe Ile Val Asp Arg Leu Lys Ser Leu Ile Lys Tyr Lys Gly  
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 Tyr Gln Val Pro Pro Ala Glu Leu Glu Ser Val Leu Leu Gln His Pro  
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 Glu Leu Pro Gly Ala Val Val Val Leu Glu Ser Gly Lys Asn Met Thr  
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 gaa aaa gaa gta atg gat tat gtt gca agt caa gtt tca aat gca aaa 1536  
 Glu Lys Glu Val Met Asp Tyr Val Ala Ser Gln Val Ser Asn Ala Lys  
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 Arg Leu Arg Gly Gly Val Arg Phe Val Asp Glu Val Pro Lys Gly Leu  
 515 520 525  
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cca aca gtt cca act tct tgt gaa gct aaa gaa gga gaa tgt ata gat Pro Thr Val Pro Thr Ser Cys Glu Ala Lys Glu Gly Glu Cys Ile Asp 35 40 45	144
acc aga tgc gca aca tgt aaa cga gat ata cta tca gat gga ctg tgt Thr Arg Cys Ala Thr Cys Lys Arg Asp Ile Leu Ser Asp Gly Leu Cys 50 55 60	192
gaa aat aaa cca ggg aag aca tgc tgt aga atg tgc cag tat gtg att Glu Asn Lys Pro Gly Lys Thr Cys Cys Arg Met Cys Gln Tyr Val Ile 65 70 75 80	240
gaa tgc aga gta gaa gca gct ggt tat ttt aga acg ttt tac ggc aaa Glu Cys Arg Val Glu Ala Ala Gly Tyr Phe Arg Thr Phe Tyr Gly Lys 85 90 95	288
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cag aag gga gct gtg ctg act aag aca aca ctg gag gtt gca gga gac Gln Lys Gly Ala Val Leu Thr Lys Thr Thr Leu Glu Val Ala Gly Asp 130 135 140	432
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gga gct gac cca gtt atc gct aac ccg ttc aca att ggt gag gtg acc Gly Ala Asp Pro Val Ile Ala Asn Pro Phe Thr Ile Gly Glu Val Thr 165 170 175	528
att gct gtt gtt gaa ata ccg ggc ttc aat atc aca gtc atc gaa ttc Ile Ala Val Val Glu Ile Pro Gly Phe Asn Ile Thr Val Ile Glu Phe 180 185 190	576
ttt aaa cta atc gtg att gat att ctg gga gga aga tct gtc aga att Phe Lys Leu Ile Val Ile Asp Ile Leu Gly Gly Arg Ser Val Arg Ile 195 200 205	624
gct cca gac aca gca aac aaa gga ctg ata tct ggt atc tgt ggt aat Ala Pro Asp Thr Ala Asn Lys Gly Leu Ile Ser Gly Ile Cys Gly Asn 210 215 220	672
ctg gag atg aat gac gct gat gac ttt act aca gat gca gat cag ctg Leu Glu Met Asn Asp Ala Asp Asp Phe Thr Thr Asp Ala Asp Gln Leu 225 230 235 240	720
gcg atc caa ccc aac ata aac aaa gag ttc gac ggc tgc cca ttc tat Ala Ile Gln Pro Asn Ile Asn Lys Glu Phe Asp Gly Cys Pro Phe Tyr 245 250 255	768
ggc aat cct tct gat atc gaa tac tgc aaa ggt ctg atg gag cca tac	816



Gly	Asn	Pro	Ser	Asp	Ile	Glu	Tyr	Cys	Lys	Gly	Leu	Met	Glu	Pro	Tyr	
			260					265					270			
aga	gct	gta	tgt	cgt	aac	aat	atc	aac	ttc	tac	tat	tac	act	cta	tcc	864
Arg	Ala	Val	Cys	Arg	Asn	Asn	Ile	Asn	Phe	Tyr	Tyr	Tyr	Thr	Leu	Ser	
		275					280					285				
tgt	gcc	ttc	gct	tac	tgt	atg	gga	gga	gaa	gaa	aga	gct	aaa	cac	gtc	912
Cys	Ala	Phe	Ala	Tyr	Cys	Met	Gly	Gly	Glu	Glu	Arg	Ala	Lys	His	Val	
	290					295					300					
ctt	ttc	gac	tat	gtt	gag	aca	tgc	gct	gcg	ccg	gaa	acg	aga	gga	acg	960
Leu	Phe	Asp	Tyr	Val	Glu	Thr	Cys	Ala	Ala	Pro	Glu	Thr	Arg	Gly	Thr	
305					310					315					320	
tgt	gtt	tta	tca	gga	cat	act	ttc	tat	gac	aca	ttc	gac	aaa	gca	aga	1008
Cys	Val	Leu	Ser	Gly	His	Thr	Phe	Tyr	Asp	Thr	Phe	Asp	Lys	Ala	Arg	
				325					330					335		
tat	caa	ttc	cag	ggc	cca	tgc	aag	gag	att	ctg	atg	gcc	gca	gac	tgt	1056
Tyr	Gln	Phe	Gln	Gly	Pro	Cys	Lys	Glu	Ile	Leu	Met	Ala	Ala	Asp	Cys	
			340					345					350			
tac	tgg	aac	aca	tgg	gat	gta	aag	gtt	tca	cat	aga	gac	gtc	gaa	tca	1104
Tyr	Trp	Asn	Thr	Trp	Asp	Val	Lys	Val	Ser	His	Arg	Asp	Val	Glu	Ser	
		355				360						365				
tac	act	gag	gta	gag	aaa	gta	aca	atc	agg	aaa	cag	tca	act	gta	gta	1152
Tyr	Thr	Glu	Val	Glu	Lys	Val	Thr	Ile	Arg	Lys	Gln	Ser	Thr	Val	Val	
	370					375					380					
gat	ctc	att	gtg	gat	ggc	aag	cag	gtc	aag	gtt	gga	gga	gtg	gat	gta	1200
Asp	Leu	Ile	Val	Asp	Gly	Lys	Gln	Val	Lys	Val	Gly	Gly	Val	Asp	Val	
385					390				395						400	
tct	atc	ccg	tac	agc	tct	gag	aac	act	tcc	ata	tac	tgg	cag	gat	gga	1248
Ser	Ile	Pro	Tyr	Ser	Ser	Glu	Asn	Thr	Ser	Ile	Tyr	Trp	Gln	Asp	Gly	
				405					410					415		
gac	atc	ctg	acg	acg	gcc	atc	cta	cct	gaa	gct	ctt	gtc	gtt	aag	ttc	1296
Asp	Ile	Leu	Thr	Thr	Ala	Ile	Leu	Pro	Glu	Ala	Leu	Val	Val	Lys	Phe	
			420					425					430			
aac	ttt	aag	cag	ctc	ctt	gta	gtt	cat	atc	aga	gat	cca	ttc	gat	gca	1344
Asn	Phe	Lys	Gln	Leu	Leu	Val	Val	His	Ile	Arg	Asp	Pro	Phe	Asp	Ala	
		435				440						445				
aag	aca	tgc	ggc	ata	tgt	ggt	aac	tat	aat	caa	gat	tca	act	gat	gat	1392
Lys	Thr	Cys	Gly	Ile	Cys	Gly	Asn	Tyr	Asn	Gln	Asp	Ser	Thr	Asp	Asp	
	450					455					460					
ttc	ttt	gac	gca	gaa	gga	gca	tgc	gct	cta	acc	ccc	aac	ccc	cca	gga	1440
Phe	Phe	Asp	Ala	Glu	Gly	Ala	Cys	Ala	Leu	Thr	Pro	Asn	Pro	Pro	Gly	
465					470					475					480	
tgt	aca	gag	gaa	cag	aaa	cca	gaa	gct	gag	cga	ctt	tgc	aat	aat	ctc	1488
Cys	Thr	Glu	Glu	Gln	Lys	Pro	Glu	Ala	Glu	Arg	Leu	Cys	Asn	Asn	Leu	
				485				490						495		
ttt	gat	tct	tct	atc	gac	gag	aaa	tgt	aat	gtc	tgc	tac	aag	cct	gac	1536
Phe	Asp	Ser	Ser	Ile	Asp	Glu	Lys	Cys	Asn	Val	Cys	Tyr	Lys	Pro	Asp	
			500					505					510			
cgg	att	gcc	cga	tgt	atg	tac	gag	tat	tgc	ctg	agg	gga	caa	caa	gga	1584
Arg	Ile	Ala	Arg	Cys	Met	Tyr	Glu	Tyr	Cys	Leu	Arg	Gly	Gln	Gln	Gly	

515	520	525	
ttt tgt gac cat gct tgg	gag ttc aag aaa gaa	tgc tac ata aaa cat	1632
Phe Cys Asp His Ala Trp	Glu Phe Lys Lys Glu	Cys Tyr Ile Lys His	
530	535	540	
gga gac act cta gaa gta	cca cct gaa tgt caa	taaacgtaca aagatacaga	1685
Gly Asp Thr Leu Glu Val	Pro Pro Glu Cys Gln		
545	550	555	
agctaaggct actacagcag	aagataaaaa agaaactgta	gttcctttcaa aaaccgtgta	1745
ttttatgtac tcattgttta	attagagcaa aataaattgt	tattatcata acttaaaacta	1805
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ttacatcaaaa tctctagt	ttg atcaactaaa ttgtctcgac	aacaacaagc aaac atg	117
		Met	
		1	
aca agc aaa caa tac tca	gtc aag ctt aca tca	gac ttc gac aac cca	165
Thr Ser Lys Gln Tyr Ser	Val Lys Leu Thr Ser	Asp Phe Asp Asn Pro	
5	10	15	
aga tgg att gga cga cac	aag cat atg ttc aat	ttc ctt gat gtc aac	213
Arg Trp Ile Gly Arg His	Lys His Met Phe Asn	Phe Leu Asp Val Asn	
20	25	30	
cac aat gga aaa atc tct	ctt gag gag atg gtc	tac aag gca tct gat	261
His Asn Gly Lys Ile Ser	Leu Asp Glu Met Val	Tyr Lys Ala Ser Asp	
35	40	45	
att gtc atc aat aac ctt	gga gca aca cct gag	caa gcc aaa cga cac	309
Ile Val Ile Asn Asn Leu	Gly Ala Thr Pro Glu	Gln Ala Lys Arg His	
50	55	60	65
aaa gat gct gta gaa gcc	ttc ttc gga gga gct	gga atg aaa tat ggt	357
Lys Asp Ala Val Glu Ala	Phe Phe Gly Gly Ala	Gly Met Lys Tyr Gly	
70	75	80	
gtg gaa act gat tgg cct	gca tat att gaa gga	tgg aaa aaa ttg gct	405
Val Glu Thr Asp Trp Pro	Ala Tyr Ile Glu Gly	Trp Lys Lys Leu Ala	
85	90	95	
act gat gaa ttg gag aaa	tac gcc aaa aac gaa	cca acg ctc atc cgt	453
Thr Asp Glu Leu Glu Lys	Tyr Ala Lys Asn Glu	Pro Thr Leu Ile Arg	
100	105	110	
ata tgg ggt gat gct ttg	ttt gat atc gtt gac	aaa gat caa aat gga	501
Ile Trp Gly Asp Ala Leu	Phe Asp Ile Val Asp	Lys Asp Gln Asn Gly	
115	120	125	
gcc att aca ctg gat gaa	tgg aaa gca tac acc	aaa gct gct ggt atc	549
Ala Ile Thr Leu Asp Glu	Trp Lys Ala Tyr Thr	Lys Ala Ala Gly Ile	
130	135	140	145

atc caa tca tca gaa gat tgc gag gaa aca ttc aga gtg tgc gat att 597  
 Ile Gln Ser Ser Glu Asp Cys Glu Glu Thr Phe Arg Val Cys Asp Ile  
 150 155 160

gat gaa agt gga caa ctc gat gtt gat gag atg aca aga caa cat tta 645  
 Asp Glu Ser Gly Gln Leu Asp Val Asp Glu Met Thr Arg Gln His Leu  
 165 170 175

gga ttt tgg tac acc atg gat cct gct tgc gaa aag ctc tac ggt gga 693  
 Gly Phe Trp Tyr Thr Met Asp Pro Ala Cys Glu Lys Leu Tyr Gly Gly  
 180 185 190

gct gtc ccc taagaagctc tacgggtggtg atgcacccta ggaagatgat 742  
 Ala Val Pro  
 195

gtgattttga ataaaacact gatgaattca atcaaaattht tccaaattht tgaacgattt 802  
 caatcggtttg tggttgatttt tgtaattagg aacagattaa atcgaatgat tagttgtttt 862  
 tttaatcaac agaacttaca aatcgaaaaa gtataaaaaa aaaaaaaaaa aaaaaaaaaa 922  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 958

<210> 6  
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 <212> DNA  
 <213> Aequorea victoria

<220>  
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 <223> Recombinant Aequorin AEQ1

<400> 6

atg acc agc gaa caa tac tca gtc aag ctt aca cca gac ttc gac aac 48  
 Met Thr Ser Glu Gln Tyr Ser Val Lys Leu Thr Pro Asp Phe Asp Asn  
 1 5 10 15

cca aaa tgg att gga cga cac aag cac atg ttt aat ttt ctt gat gtc 96  
 Pro Lys Trp Ile Gly Arg His Lys His Met Phe Asn Phe Leu Asp Val  
 20 25 30

aac cac aat gga agg atc tct ctt gac gag atg gtc tac aag gcg tcc 144  
 Asn His Asn Gly Arg Ile Ser Leu Asp Glu Met Val Tyr Lys Ala Ser  
 35 40 45

gat att gtt ata aac aat ctt gga gca aca cct gaa caa gcc aaa cgt 192  
 Asp Ile Val Ile Asn Asn Leu Gly Ala Thr Pro Glu Gln Ala Lys Arg  
 50 55 60

cac aaa gat gct gta gaa gcc ttc ttc gga gga gct gga atg aaa tat 240  
 His Lys Asp Ala Val Glu Ala Phe Phe Gly Gly Ala Gly Met Lys Tyr  
 65 70 75 80

ggt gta gaa act gaa tgg cct gaa tac atc gaa gga tgg aaa aga ctg 288  
 Gly Val Glu Thr Glu Trp Pro Glu Tyr Ile Glu Gly Trp Lys Arg Leu  
 85 90 95

gct tcc gag gaa ttg aaa agg tat tca aaa aac caa atc aca ctt att 336  
 Ala Ser Glu Glu Leu Lys Arg Tyr Ser Lys Asn Gln Ile Thr Leu Ile  
 100 105 110

cgt tta tgg ggt gat gca ttg ttc gat atc att gac aaa gac caa aat 384  
 Arg Leu Trp Gly Asp Ala Leu Phe Asp Ile Ile Asp Lys Asp Gln Asn  
 115 120 125

gga gct att tca ctg gat gaa tgg aaa gca tac acc aaa tct gat ggc	432
Gly Ala Ile Ser Leu Asp Glu Trp Lys Ala Tyr Thr Lys Ser Asp Gly	
130 135 140	
atc atc caa tcg tca gaa gat tgc gag gaa aca ttc aga gtg tgc gat	480
Ile Ile Gln Ser Ser Glu Asp Cys Glu Glu Thr Phe Arg Val Cys Asp	
145 150 155 160	
att gat gaa agt gga cag ctc gat gtt gat gag atg aca aga caa cat	528
Ile Asp Glu Ser Gly Gln Leu Asp Val Asp Glu Met Thr Arg Gln His	
165 170 175	
tta gga ttt tgg tac acc atg gat cct gct tgc gaa aag ctc tac ggt	576
Leu Gly Phe Trp Tyr Thr Met Asp Pro Ala Cys Glu Lys Leu Tyr Gly	
180 185 190	
gga gct gtc ccc taa	591
Gly Ala Val Pro	
195	

<210> 7  
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 <220>  
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Met Thr Ser Glu Gln Tyr Ser Val Lys Leu Thr Ser Asp Phe Asn	
1 5 10 15	
cca aga tgg att gga cga cac aag cat atg ttc aat ttc ctt gat gtc	96
Pro Arg Trp Ile Gly Arg His Lys His Met Phe Asn Phe Leu Asp Val	
20 25 30	
aac cac aat gga aaa atc tct ctt gac gag atg gtc tac aag gca tct	144
Asn His Asn Gly Lys Ile Ser Leu Asp Glu Met Val Tyr Lys Ala Ser	
35 40 45	
gat att gtc atc aat aac ctt gga gca aca cct gag caa gcc aaa cga	192
Asp Ile Val Ile Asn Asn Leu Gly Ala Thr Pro Glu Gln Ala Lys Arg	
50 55 60	
cac aaa gat gct gta gaa gcc ttc ttc gga gga gct gga atg aaa tat	240
His Lys Asp Ala Val Glu Ala Phe Phe Gly Gly Ala Gly Met Lys Tyr	
65 70 75 80	
ggg gtg gaa act gat tgg cct gca tat att gaa gga tgg aaa aaa ttg	288
Gly Val Glu Thr Asp Trp Pro Ala Tyr Ile Glu Gly Trp Lys Lys Leu	
85 90 95	
gct act gat gaa ttg gag aaa tac gcc aaa aac gaa cca acg ctc atc	336
Ala Thr Asp Glu Leu Glu Lys Tyr Ala Lys Asn Glu Pro Thr Leu Ile	
100 105 110	
cgt ata tgg ggt gat gct ttg ttc gat atc gtt gac aaa gat caa aat	384
Arg Ile Trp Gly Asp Ala Leu Phe Asp Ile Val Asp Lys Asp Gln Asn	
115 120 125	

gga gcc att aca ctg gat gaa tgg aaa gca tac acc aaa gct gct ggt 432  
 Gly Ala Ile Thr Leu Asp Glu Trp Lys Ala Tyr Thr Lys Ala Ala Gly  
       130                      135                      140

atc atc caa tca tca gaa gat tgc gag gaa aca ttc aga gtg tgc gat 480  
 Ile Ile Gln Ser Ser Glu Asp Cys Glu Glu Thr Phe Arg Val Cys Asp  
       145                      150                      155                      160

att gat gaa agt gga caa ctc gat gtt gat gag atg aca aga caa cat 528  
 Ile Asp Glu Ser Gly Gln Leu Asp Val Asp Glu Met Thr Arg Gln His  
                       165                      170                      175

tta gga ttt tgg tac acc atg gat cct gct tgc gaa aag ctc tac ggt 576  
 Leu Gly Phe Trp Tyr Thr Met Asp Pro Ala Cys Glu Lys Leu Tyr Gly  
                       180                      185                      190

gga gct gtc ccc taa 591  
 Gly Ala Val Pro  
       195

<210> 8  
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 <212> DNA  
 <213> Aequoria victoria

<220>  
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 <223> Recombinant Aequorin AEQ3

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 Met Thr Ser Glu Gln Tyr Ser Val Lys Leu Thr Ser Asp Phe Asp Asn  
       1                      5                      10                      15

cca aga tgg att gga cga cac aag cat atg ttc aat ttc ctt gat gtc 96  
 Pro Arg Trp Ile Gly Arg His Lys His Met Phe Asn Phe Leu Asp Val  
                       20                      25                      30

aac cac aat gga aaa atc tct ctt gac gag atg gtc tac aag gca tct 144  
 Asn His Asn Gly Lys Ile Ser Leu Asp Glu Met Val Tyr Lys Ala Ser  
                       35                      40                      45

gat att gtc atc aat aac ctt gga gca aca cct gag caa gcc aaa cga 192  
 Asp Ile Val Ile Asn Asn Leu Gly Ala Thr Pro Glu Gln Ala Lys Arg  
       50                      55                      60

cac aaa gat gct gta gga gac ttc ttc gga gga gct gga atg aaa tat 240  
 His Lys Asp Ala Val Gly Asp Phe Phe Gly Gly Ala Gly Met Lys Tyr  
       65                      70                      75                      80

ggt gtg gaa act gat tgg cct gca tac att gaa gga tgg aaa aaa ttg 288  
 Gly Val Glu Thr Asp Trp Pro Ala Tyr Ile Glu Gly Trp Lys Lys Leu  
                       85                      90                      95

gct act gat gaa ttg gag aaa tac gcc aaa aac gaa cca acg ctc atc 336  
 Ala Thr Asp Glu Leu Glu Lys Tyr Ala Lys Asn Glu Pro Thr Leu Ile  
       100                      105                      110

cgt ata tgg ggt gat gct ttg ttc gat atc gtt gac aaa gat caa aat 384  
 Arg Ile Trp Gly Asp Ala Leu Phe Asp Ile Val Asp Lys Asp Gln Asn  
       115                      120                      125

gga gcc att aca ctg gat gaa tgg aaa gca tac acc aaa gct gct ggt 432

Gly	Ala	Ile	Thr	Leu	Asp	Glu	Trp	Lys	Ala	Tyr	Thr	Lys	Ala	Ala	Gly		
130						135					140						
atc	atc	caa	tca	tca	gaa	gat	tgc	gag	gaa	aca	ttc	aga	gtg	tgc	gat	480	
Ile	Ile	Gln	Ser	Ser	Glu	Asp	Cys	Glu	Glu	Thr	Phe	Arg	Val	Cys	Asp		
145					150				155					160			
att	gat	gaa	aat	gga	caa	ctc	gat	gtt	gat	gag	atg	aca	aga	caa	cat	528	
Ile	Asp	Glu	Asn	Gly	Gln	Leu	Asp	Val	Asp	Glu	Met	Thr	Arg	Gln	His		
				165				170						175			
tta	gga	ttt	tgg	tac	acc	atg	gat	cct	gct	tgc	gaa	aag	ctc	tac	ggc	576	
Leu	Gly	Phe	Trp	Tyr	Thr	Met	Asp	Pro	Ala	Cys	Glu	Lys	Leu	Tyr	Gly		
			180					185					190				
gga	gct	gtc	ccc	taa												591	
Gly	Ala	Val	Pro														
			195														
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Val	Lys	Leu	Thr	Pro	Asp	Phe	Asp	Asn	Pro	Lys	Trp	Ile	Gly	Arg	His		
1				5				10						15			
aag	cac	atg	ttt	aat	ttt	ctt	gat	gtc	aac	cac	aat	gga	agg	atc	tct	96	
Lys	His	Met	Phe	Asn	Phe	Leu	Asp	Val	Asn	His	Asn	Gly	Arg	Ile	Ser		
			20					25					30				
ctt	gac	gag	atg	gtc	tac	aag	gcg	tcc	gat	att	gtt	ata	aac	aat	ctt	144	
Leu	Asp	Glu	Met	Val	Tyr	Lys	Ala	Ser	Asp	Ile	Val	Ile	Asn	Asn	Leu		
			35				40					45					
gga	gca	aca	cct	gaa	caa	gcc	aaa	cgt	cac	aaa	gat	gct	gta	gaa	gcc	192	
Gly	Ala	Thr	Pro	Glu	Gln	Ala	Lys	Arg	His	Lys	Asp	Ala	Val	Glu	Ala		
			50			55					60						
ttc	ttc	gga	gga	gct	gca	atg	aaa	tat	ggt	gta	gaa	act	gaa	tgg	cct	240	
Phe	Phe	Gly	Gly	Ala	Ala	Met	Lys	Tyr	Gly	Val	Glu	Thr	Glu	Trp	Pro		
65				70					75					80			
gaa	tac	atc	gaa	gga	tgg	aaa	aga	ctg	gct	tcc	gag	gaa	ttg	aaa	agg	288	
Glu	Tyr	Ile	Glu	Gly	Trp	Lys	Arg	Leu	Ala	Ser	Glu	Glu	Leu	Lys	Arg		
			85					90						95			
tat	tca	aaa	aac	caa	atc	aca	ctt	att	cgt	tta	tgg	ggt	gat	gca	ttg	336	
Tyr	Ser	Lys	Asn	Gln	Ile	Thr	Leu	Ile	Arg	Leu	Trp	Gly	Asp	Ala	Leu		
			100				105						110				
ttc	gat	atc	att	gac	aaa	gac	caa	aat	gga	gct	att	tca	ctg	gat	gaa	384	
Phe	Asp	Ile	Ile	Asp	Lys	Asp	Gln	Asn	Gly	Ala	Ile	Ser	Leu	Asp	Glu		
			115				120					125					
tgg	aaa	gca	tac	acc	aaa	tct	gct	ggc	atc	atc	caa	tcg	tca	gaa	gat	432	
Trp	Lys	Ala	Tyr	Thr	Lys	Ser	Ala	Gly	Ile	Ile	Gln	Ser	Ser	Glu	Asp		
			130			135					140						

tgc gag gaa aca ttc aga gtg tgc gat att gat gaa agt gga cag ctc 480  
 Cys Glu Glu Thr Phe Arg Val Cys Asp Ile Asp Glu Ser Gly Gln Leu  
 145 150 155 160

gat gtt gat gag atg aca aga caa cat tta gga ttt tgg tac acc atg 528  
 Asp Val Asp Glu Met Thr Arg Gln His Leu Gly Phe Trp Tyr Thr Met  
 165 170 175

gat cct gct tgc gaa aag ctc tac ggt gga gct gtc ccc 567  
 Asp Pro Ala Cys Glu Lys Leu Tyr Gly Gly Ala Val Pro  
 180 185

<210> 10

<211> 588

<212> DNA

<213> Aequoria victoria

<220>

<221> CDS

<222> (1)...(588)

<223> Aequorin mutant w/increased bioluminescence  
 activity

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 Met Thr Ser Glu Gln Tyr Ser Val Lys Leu Thr Pro Asp Phe Asp Asn  
 1 5 10 15

cca aaa tgg att gga cga cac aag cac atg ttt aat ttt ctt gat gtc 96  
 Pro Lys Trp Ile Gly Arg His Lys His Met Phe Asn Phe Leu Asp Val  
 20 25 30

aac cac aat gga agg atc tct ctt gac gag atg gtc tac aag gcg tcc 144  
 Asn His Asn Gly Arg Ile Ser Leu Asp Glu Met Val Tyr Lys Ala Ser  
 35 40 45

gat att gtt ata aac aat ctt gga gca aca cct gaa caa gcc aaa cgt 192  
 Asp Ile Val Ile Asn Asn Leu Gly Ala Thr Pro Glu Gln Ala Lys Arg  
 50 55 60

cac aaa gat gct gta gaa gcc ttc ttc gga gga gct gca atg aaa tat 240  
 His Lys Asp Ala Val Glu Ala Phe Phe Gly Gly Ala Ala Met Lys Tyr  
 65 70 75 80

ggt gta gaa act gaa tgg cct gaa tac atc gaa gga tgg aaa aga ctg 288  
 Gly Val Glu Thr Glu Trp Pro Glu Tyr Ile Glu Gly Trp Lys Arg Leu  
 85 90 95

gct tcc gag gaa ttg aaa agg tat tca aaa aac caa atc aca ctt att 336  
 Ala Ser Glu Glu Leu Lys Arg Tyr Ser Lys Asn Gln Ile Thr Leu Ile  
 100 105 110

cgt tta tgg ggt gat gca ttg ttc gat atc att tcc aaa gac caa aat 384  
 Arg Leu Trp Gly Asp Ala Leu Phe Asp Ile Ile Ser Lys Asp Gln Asn  
 115 120 125

gga gct att tca ctg gat gaa tgg aaa gca tac acc aaa tct gct ggc 432  
 Gly Ala Ile Ser Leu Asp Glu Trp Lys Ala Tyr Thr Lys Ser Ala Gly  
 130 135 140

atc atc caa tcg tca gaa gat tgc gag gaa aca ttc aga gtg tgc gat 480  
 Ile Ile Gln Ser Ser Glu Asp Cys Glu Glu Thr Phe Arg Val Cys Asp  
 145 150 155 160

att gat gaa agt gga cag ctc gat gtt gat gag atg aca aga caa cat 528  
 Ile Asp Glu Ser Gly Gln Leu Asp Val Asp Glu Met Thr Arg Gln His  
 165 170 175

tta gga ttt tgg tac acc atg gat cct gct tgc gaa aag ctc tac ggt 576  
 Leu Gly Phe Trp Tyr Thr Met Asp Pro Ala Cys Glu Lys Leu Tyr Gly  
 180 185 190

gga gct gtc ccc 588  
 Gly Ala Val Pro  
 195

<210> 11

<211> 588

<212> DNA

<213> Aequarea victoria

<220>

<221> CDS

<222> (1)...(588)

<223> Recombinant site-directed Aequarein mutant

<400> 11

atg acc agc gaa caa tac tca gtc aag ctt aca cca gac ttc gac aac 48  
 Met Thr Ser Glu Gln Tyr Ser Val Lys Leu Thr Pro Asp Phe Asp Asn  
 1 5 10 15

cca aaa tgg att gga cga cac aag cac atg ttt aat ttt ctt gat gtc 96  
 Pro Lys Trp Ile Gly Arg His Lys His Met Phe Asn Phe Leu Asp Val  
 20 25 30

aac cac aat gga agg atc tct ctt gac gag atg gtc tac aag gcg tcc 144  
 Asn His Asn Gly Arg Ile Ser Leu Asp Glu Met Val Tyr Lys Ala Ser  
 35 40 45

gat att gtt ata aac aat ctt gga gca aca cct gaa caa gcc aaa cgt 192  
 Asp Ile Val Ile Asn Asn Leu Gly Ala Thr Pro Glu Gln Ala Lys Arg  
 50 55 60

cac aaa gat gct gta gaa gcc ttc ttc gga gga gct gca atg aaa tat 240  
 His Lys Asp Ala Val Glu Ala Phe Phe Gly Gly Ala Ala Met Lys Tyr  
 65 70 75 80

ggt gta gaa act gaa tgg cct gaa tac atc gaa gga tgg aaa aga ctg 288  
 Gly Val Glu Thr Glu Trp Pro Glu Tyr Ile Glu Gly Trp Lys Arg Leu  
 85 90 95

gct tcc gag gaa ttg aaa agg tat tca aaa aac caa atc aca ctt att 336  
 Ala Ser Glu Glu Leu Lys Arg Tyr Ser Lys Asn Gln Ile Thr Leu Ile  
 100 105 110

cgt tta tgg ggt gat gca ttg ttc gat atc att tcc aaa gac caa aat 384  
 Arg Leu Trp Gly Asp Ala Leu Phe Asp Ile Ile Ser Lys Asp Gln Asn  
 115 120 125

gga gct att tca ctg gat tca tgg aaa gca tac acc aaa tct gct ggc 432  
 Gly Ala Ile Ser Leu Asp Ser Trp Lys Ala Tyr Thr Lys Ser Ala Gly  
 130 135 140

atc atc caa tcg tca gaa gat tgc gag gaa aca ttc aga gtg tgc gat 480  
 Ile Ile Gln Ser Ser Glu Asp Cys Glu Glu Thr Phe Arg Val Cys Asp  
 145 150 155 160



att gat gaa agt gga cag ctc gat gtt gat gag atg aca aga caa cat 528  
 Ile Asp Glu Ser Gly Gln Leu Asp Val Asp Glu Met Thr Arg Gln His  
                   165                                  170                                  175

tta gga ttt tgg tac acc atg gat cct gct tgc gaa aag ctc tac ggt 576  
 Leu Gly Phe Trp Tyr Thr Met Asp Pro Ala Cys Glu Lys Leu Tyr Gly  
                   180                                  185                                  190

gga gct gtc ccc 588  
 Gly Ala Val Pro  
                   195

<210> 12

<211> 588

<212> DNA

<213> Aequorea victoria

<220>

<221> CDS

<222> (1)...(588)

<223> Aequorin mutant with increased bioluminescence activity

<400> 12

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 Met Thr Ser Glu Gln Tyr Ser Val Lys Leu Thr Pro Asp Phe Asp Asn  
                   1                                  5                                  10                                  15

cca aaa tgg att gga cga cac aag cac atg ttt aat ttt ctt gat gtc 96  
 Pro Lys Trp Ile Gly Arg His Lys His Met Phe Asn Phe Leu Asp Val  
                   20                                  25                                  30

aac cac aat gga agg atc tct ctt gac gag atg gtc tac aag gcg tcc 144  
 Asn His Asn Gly Arg Ile Ser Leu Asp Glu Met Val Tyr Lys Ala Ser  
                   35                                  40                                  45

gat att gtt ata aac aat ctt gga gca aca cct gaa caa gcc aaa cgt 192  
 Asp Ile Val Ile Asn Asn Leu Gly Ala Thr Pro Glu Gln Ala Lys Arg  
                   50                                  55                                  60

cac aaa gat gct gta gaa gcc ttc ttc gga gga gct gca atg aaa tat 240  
 His Lys Asp Ala Val Glu Ala Phe Phe Gly Gly Ala Ala Met Lys Tyr  
                   65                                  70                                  75                                  80

ggg gta gaa act gaa tgg cct gaa tac atc gaa gga tgg aaa aga ctg 288  
 Gly Val Glu Thr Glu Trp Pro Glu Tyr Ile Glu Gly Trp Lys Arg Leu  
                   85                                  90                                  95

gct tcc gag gaa ttg aaa agg tat tca aaa aac caa atc aca ctt att 336  
 Ala Ser Glu Glu Leu Lys Arg Tyr Ser Lys Asn Gln Ile Thr Leu Ile  
                   100                                  105                                  110

cgt tta tgg ggt gat gca ttg ttc gat atc att tcc aaa gac caa aat 384  
 Arg Leu Trp Gly Asp Ala Leu Phe Asp Ile Ile Ser Lys Asp Gln Asn  
                   115                                  120                                  125

gca gct att tca ctg gat gaa tgg aaa gca tac acc aaa tct gct ggc 432  
 Ala Ala Ile Ser Leu Asp Glu Trp Lys Ala Tyr Thr Lys Ser Ala Gly  
                   130                                  135                                  140

atc atc caa tcg tca gaa gat tgc gag gaa aca ttc aga gtg tgc gat 480  
 Ile Ile Gln Ser Ser Glu Asp Cys Glu Glu Thr Phe Arg Val Cys Asp  
                   145                                  150                                  155                                  160

att gat gaa agt gga cag ctc gat gtt gat gag atg aca aga caa cat 528  
 Ile Asp Glu Ser Gly Gln Leu Asp Val Asp Glu Met Thr Arg Gln His  
 165 170 175

tta gga ttt tgg tac acc atg gat cct gct tgc gaa aag ctc tac ggt 576  
 Leu Gly Phe Trp Tyr Thr Met Asp Pro Ala Cys Glu Lys Leu Tyr Gly  
 180 185 190

gga gct gtc ccc 588  
 Gly Ala Val Pro  
 195

<210> 13  
 <211> 567  
 <212> DNA  
 <213> Aequorea victoria

<220>  
 <221> CDS  
 <222> (1)...(567)  
 <223> Recombinant apoaequorin (AQUALITEp)

<400> 13

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 Val Lys Leu Thr Pro Asp Phe Asp Asn Pro Lys Trp Ile Gly Arg His  
 1 5 10 15

aag cac atg ttt aat ttt ctt gat gtc aac cac aat gga agg atc tct 96  
 Lys His Met Phe Asn Phe Leu Asp Val Asn His Asn Gly Arg Ile Ser  
 20 25 30

ctt gac gag atg gtc tac aag gcg tcc gat att gtt ata aac aat ctt 144  
 Leu Asp Glu Met Val Tyr Lys Ala Ser Asp Ile Val Ile Asn Asn Leu  
 35 40 45

gga gca aca cct gaa caa gcc aaa cgt cac aaa gat gct gta gaa gcc 192  
 Gly Ala Thr Pro Glu Gln Ala Lys Arg His Lys Asp Ala Val Glu Ala  
 50 55 60

ttc ttc gga gga gct gga atg aaa tat ggt gta gaa act gaa tgg cct 240  
 Phe Phe Gly Gly Ala Gly Met Lys Tyr Gly Val Glu Thr Glu Trp Pro  
 65 70 75 80

gaa tac atc gaa gga tgg aaa aaa ctg gct tcc gag gaa ttg aaa agg 288  
 Glu Tyr Ile Glu Gly Trp Lys Lys Leu Ala Ser Glu Glu Leu Lys Arg  
 85 90 95

tat tca aaa aac caa atc aca ctt att cgt tta tgg ggt gat gca ttg 336  
 Tyr Ser Lys Asn Gln Ile Thr Leu Ile Arg Leu Trp Gly Asp Ala Leu  
 100 105 110

ttc gat atc att gac aaa gac caa aat gga gct att ctg tca gat gaa 384  
 Phe Asp Ile Ile Asp Lys Asp Gln Asn Gly Ala Ile Leu Ser Asp Glu  
 115 120 125

tgg aaa gca tac acc aaa tct gat ggc atc atc caa tcg tca gaa gat 432  
 Trp Lys Ala Tyr Thr Lys Ser Asp Gly Ile Ile Gln Ser Ser Glu Asp  
 130 135 140

tgc gag gaa aca ttc aga gtg tgc gat att gat gaa agt gga cag ctc 480  
 Cys Glu Glu Thr Phe Arg Val Cys Asp Ile Asp Glu Ser Gly Gln Leu  
 145 150 155 160

gat gtt gat gag atg aca aga caa cat tta gga ttt tgg tac acc atg 528

Asp Val Asp Glu Met Thr Arg Gln His Leu Gly Phe Trp Tyr Thr Met  
 165 170 175

gat cct gct tgc gaa aag ctc tac ggt gga gct gtc ccc  
 Asp Pro Ala Cys Glu Lys Leu Tyr Gly Gly Ala Val Pro  
 180 185

567

<210> 14  
 <211> 236  
 <212> PRT  
 <213> *Vibrio fisheri*

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 20 25 30  
 Gly Gln Tyr Leu Thr Val Val Met Gly Glu Lys Asp Lys Arg Pro Phe  
 35 40 45  
 Ser Ile Ala Ser Ser Pro Cys Arg His Glu Gly Glu Ile Glu Leu His  
 50 55 60  
 Ile Gly Ala Ala Glu His Asn Ala Tyr Ala Gly Glu Val Val Glu Ser  
 65 70 75 80  
 Met Lys Ser Ala Leu Glu Thr Gly Gly Asp Ile Leu Ile Asp Ala Pro  
 85 90 95  
 His Gly Glu Ala Trp Ile Arg Glu Asp Ser Asp Arg Ser Met Leu Leu  
 100 105 110  
 Ile Ala Gly Thr Gly Phe Ser Tyr Val Arg Ser Ile Leu Asp His  
 115 120 125  
 Cys Ile Ser Gln Gln Ile Gln Lys Pro Ile Tyr Leu Tyr Trp Gly Gly  
 130 135 140  
 Arg Asp Glu Cys Gln Leu Tyr Ala Lys Ala Glu Leu Glu Ser Ile Ala  
 145 150 155 160  
 Gln Ala His Ser His Ile Thr Phe Val Pro Val Val Glu Lys Ser Glu  
 165 170 175  
 Gly Trp Thr Gly Lys Thr Gly Asn Val Leu Glu Ala Val Lys Ala Asp  
 180 185 190  
 Phe Asn Ser Leu Ala Asp Met Asp Ile Tyr Ile Ala Gly Arg Phe Glu  
 195 200 205  
 Met Ala Gly Ala Ala Arg Glu Gln Phe Thr Thr Glu Lys Gln Ala Lys  
 210 215 220  
 Lys Glu Gln Leu Phe Gly Asp Ala Phe Ala Phe Ile  
 225 230 235

<210> 15  
 <211> 1079  
 <212> DNA  
 <213> *Renilla mulleri*

<220>  
 <221> CDS  
 <222> (259)...(975)  
 <223> *Renilla mulleri* GFP

<400> 15  
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 gtattttacgt cagacctgtc taatcgaaac cacaacaaac tcttaaaata agccacattt 120  
 acataatatc taagagacgc ctcatTTaag agtagtaaaa atataatata tgatagagta 180  
 tacaactctc gccttagaca gacagtgtgc aacagagtaa ctcttgTTaa tgcaatcgaa 240  
 agcgtcaaga gagataag atg agt aaa caa ata ttg aag aac act tgt tta 291  
 Met Ser Lys Gln Ile Leu Lys Asn Thr Cys Leu  
 1 5 10

caa gaa gta atg tcg tat aaa gta aat ctg gaa gga att gta aac aac 339  
 Gln Glu Val Met Ser Tyr Lys Val Asn Leu Glu Gly Ile Val Asn Asn  
 15 20 25

cat gtt ttt aca atg gag ggt tgc ggc aaa ggg aat att tta ttc ggc 387  
 His Val Phe Thr Met Glu Gly Cys Gly Lys Gly Asn Ile Leu Phe Gly  
 30 35 40

aat caa ctg gtt cag att cgt gtc acg aaa ggg gcc cca ctg cct ttt 435  
 Asn Gln Leu Val Gln Ile Arg Val Thr Lys Gly Ala Pro Leu Pro Phe  
 45 50 55

gca ttt gat att gtg tca cca gct ttt caa tat ggc aac cgt act ttc 483  
 Ala Phe Asp Ile Val Ser Pro Ala Phe Gln Tyr Gly Asn Arg Thr Phe  
 60 65 70 75

acg aaa tat ccg aat gat ata tca gat tat ttt ata caa tca ttt cca 531  
 Thr Lys Tyr Pro Asn Asp Ile Ser Asp Tyr Phe Ile Gln Ser Phe Pro  
 80 85 90

gca gga ttt atg tat gaa cga aca tta cgt tac gaa gat ggc gga ctt 579  
 Ala Gly Phe Met Tyr Glu Arg Thr Leu Arg Tyr Glu Asp Gly Gly Leu  
 95 100 105

gtt gaa att cgt tca gat ata aat tta ata gaa gac aag ttc gtc tac 627  
 Val Glu Ile Arg Ser Asp Ile Asn Leu Ile Glu Asp Lys Phe Val Tyr  
 110 115 120

aga gtg gaa tac aaa ggt agt aac ttc cca gat gat ggt ccc gtc atg 675  
 Arg Val Glu Tyr Lys Gly Ser Asn Phe Pro Asp Asp Gly Pro Val Met  
 125 130 135

cag aag act atc tta gga ata gag cct tca ttt gaa gcc atg tac atg 723  
 Gln Lys Thr Ile Leu Gly Ile Glu Pro Ser Phe Glu Ala Met Tyr Met  
 140 145 150 155

aat aat ggc gtc ttg gtc ggc gaa gta att ctt gtc tat aaa cta aac 771  
 Asn Asn Gly Val Leu Val Gly Glu Val Ile Leu Val Tyr Lys Leu Asn  
 160 165 170

tct ggg aaa tat tat tca tgt cac atg aaa aca tta atg aag tcg aaa 819  
 Ser Gly Lys Tyr Tyr Ser Cys His Met Lys Thr Leu Met Lys Ser Lys  
 175 180 185

ggt gta gta aag gag ttt cct tcg tat cat ttt att caa cat cgt ttg 867  
 Gly Val Val Lys Glu Phe Pro Ser Tyr His Phe Ile Gln His Arg Leu  
 190 195 200

gaa aag act tac gta gaa gac ggg ggg ttc gtt gaa cag cat gag act 915  
 Glu Lys Thr Tyr Val Glu Asp Gly Gly Phe Val Glu Gln His Glu Thr  
 205 210 215

gct att gct caa atg aca tct ata gga aaa cca cta gga tcc tta cac 963  
 Ala Ile Ala Gln Met Thr Ser Ile Gly Lys Pro Leu Gly Ser Leu His  
 220 225 230 235

gaa tgg gtt taa acacagttac attacttttt ccaattcgtg tttcatgtca 1015  
 Glu Trp Val \*

aataataatt ttttaaacia ttatcaatgt tttgtgatat gtttgtaaaa aaaaaaaaaa 1075  
 aaaa 1079

<210> 16  
 <211> 238

&lt;212&gt; PRT

&lt;213&gt; Renilla mulleri

&lt;400&gt; 16

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Met Ser Lys Gln Ile Leu Lys Asn Thr Cys Leu Gln Glu Val Met Ser
1      5      10      15
Tyr Lys Val Asn Leu Glu Gly Ile Val Asn Asn His Val Phe Thr Met
20      25      30
Glu Gly Cys Gly Lys Gly Asn Ile Leu Phe Gly Asn Gln Leu Val Gln
35      40      45
Ile Arg Val Thr Lys Gly Ala Pro Leu Pro Phe Ala Phe Asp Ile Val
50      55      60
Ser Pro Ala Phe Gln Tyr Gly Asn Arg Thr Phe Thr Lys Tyr Pro Asn
65      70      75      80
Asp Ile Ser Asp Tyr Phe Ile Gln Ser Phe Pro Ala Gly Phe Met Tyr
85      90      95
Glu Arg Thr Leu Arg Tyr Glu Asp Gly Gly Leu Val Glu Ile Arg Ser
100     105     110
Asp Ile Asn Leu Ile Glu Asp Lys Phe Val Tyr Arg Val Glu Tyr Lys
115     120     125
Gly Ser Asn Phe Pro Asp Asp Gly Pro Val Met Gln Lys Thr Ile Leu
130     135     140
Gly Ile Glu Pro Ser Phe Glu Ala Met Tyr Met Asn Asn Gly Val Leu
145     150     155     160
Val Gly Glu Val Ile Leu Val Tyr Lys Leu Asn Ser Gly Lys Tyr Tyr
165     170     175
Ser Cys His Met Lys Thr Leu Met Lys Ser Lys Gly Val Val Lys Glu
180     185     190
Phe Pro Ser Tyr His Phe Ile Gln His Arg Leu Glu Lys Thr Tyr Val
195     200     205
Glu Asp Gly Gly Phe Val Glu Gln His Glu Thr Ala Ile Ala Gln Met
210     215     220
Thr Ser Ile Gly Lys Pro Leu Gly Ser Leu His Glu Trp Val
225     230     235

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&lt;210&gt; 17

&lt;211&gt; 1217

&lt;212&gt; DNA

&lt;213&gt; Renilla mulleri

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (31)...(963)

&lt;223&gt; Renilla mulleri luciferase

&lt;400&gt; 17

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cggcacgagg tttaagaatc aataaaaaaa atg acg tca aaa gtt tac gat cct      54
                        Met Thr Ser Lys Val Tyr Asp Pro
                        1      5

gaa tta aga aaa cgc atg att act ggt cca caa tgg tgg gca aga tgt      102
Glu Leu Arg Lys Arg Met Ile Thr Gly Pro Gln Trp Trp Ala Arg Cys
10      15      20

aaa caa atg aat gtt ctt gat tca ttt att aat tat tat gat tca gaa      150
Lys Gln Met Asn Val Leu Asp Ser Phe Ile Asn Tyr Tyr Asp Ser Glu
25      30      35      40

aaa cat gca gaa aat gca gtt ata ttt tta cat ggt aat gca gca tct      198
Lys His Ala Glu Asn Ala Val Ile Phe Leu His Gly Asn Ala Ala Ser
45      50      55

tct tat tta tgg cgt cat gtt gta cca cat gtt gaa cca gtg gcg cga      246
Ser Tyr Leu Trp Arg His Val Val Pro His Val Glu Pro Val Ala Arg
60      65      70

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tgt att ata cca gat ctt ata ggt atg ggt aaa tca ggc aag tct ggt	294
Cys Ile Ile Pro Asp Leu Ile Gly Met Gly Lys Ser Gly Lys Ser Gly	
75 80 85	
aat ggt tcc tat aga tta cta gat cat tac aaa tat ctt act gaa tgg	342
Asn Gly Ser Tyr Arg Leu Leu Asp His Tyr Lys Tyr Leu Thr Glu Trp	
90 95 100	
ttc aaa cat ctt aat tta cca aag aag atc att ttt gtc ggt cat gat	390
Phe Lys His Leu Asn Leu Pro Lys Lys Ile Ile Phe Val Gly His Asp	
105 110 115 120	
tgg ggt gct tgt tta gca ttt cat tat tgc tat gaa cat cag gat cgc	438
Trp Gly Ala Cys Leu Ala Phe His Tyr Cys Tyr Glu His Gln Asp Arg	
125 130 135	
atc aaa gca gtt gtt cat gct gaa agt gta gta gat gtg att gaa tcg	486
Ile Lys Ala Val Val His Ala Glu Ser Val Val Asp Val Ile Glu Ser	
140 145 150	
tgg gac gaa tgg cct gat att gaa gaa gat att gct ttg att aaa tct	534
Trp Asp Glu Trp Pro Asp Ile Glu Glu Asp Ile Ala Leu Ile Lys Ser	
155 160 165	
gaa gaa gga gaa aaa atg gtt tta gag aat aac ttc ttc gtg gaa acc	582
Glu Glu Gly Glu Lys Met Val Leu Glu Asn Asn Phe Phe Val Glu Thr	
170 175 180	
atg ttg cca tca aaa atc atg aga aag ttg gaa cca gag gaa ttt gct	630
Met Leu Pro Ser Lys Ile Met Arg Lys Leu Glu Pro Glu Glu Phe Ala	
185 190 195 200	
gct tat ctt gaa cca ttt aaa gag aaa ggt gaa gtt cgt cgt cca aca	678
Ala Tyr Leu Glu Glu Pro Phe Lys Glu Lys Gly Glu Val Arg Arg Pro Thr	
205 210 215	
tta tca tgg cct cgt gaa atc cct ttg gta aaa ggt ggt aaa ccg gat	726
Leu Ser Trp Pro Arg Glu Ile Pro Leu Val Lys Gly Gly Lys Pro Asp	
220 225 230	
gta gta gaa att gtc agg aat tat aat gct tat ctt cgt gca agt cat	774
Val Val Glu Ile Val Arg Asn Tyr Asn Ala Tyr Leu Arg Ala Ser His	
235 240 245	
gat tta cca aaa atg ttt att gaa tct gat cca gga ttc ttt tcc aat	822
Asp Leu Pro Lys Met Phe Ile Glu Ser Asp Pro Gly Phe Phe Ser Asn	
250 255 260	
gct att gtt gaa ggt gct aag aaa ttc cct aat act gaa ttt gtt aaa	870
Ala Ile Val Glu Gly Ala Lys Lys Phe Pro Asn Thr Glu Phe Val Lys	
265 270 275 280	
gtc aaa ggt ctt cat ttt tca caa gaa gat gca cct gat gaa atg gga	918
Val Lys Gly Leu His Phe Ser Gln Glu Asp Ala Pro Asp Glu Met Gly	
285 290 295	
aat tat ata aaa tcg ttt gtt gag cgt gtt ctt aaa aat gaa caa	963
Asn Tyr Ile Lys Ser Phe Val Glu Arg Val Leu Lys Asn Glu Gln	
300 305 310	
taaactacca gggtttccatg ttgccacttt agctggggttt aataaatttc actatcaatt	1023
tgaacaattt cacattaatt ttaactatta aaaaattatg gacacagggg ttatatcaga	1083
tgattaattt agttgggaac aatgaatacc gaatattatg aattctcttt agctatttat	1143
aataatcaca ttcttatgta ataaaacttt gttttaataa attaattgatt cagaaaaaaa	1203

aaaaaaaaaa aaaa

1217

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 <211> 311  
 <212> PRT  
 <213> Renilla mulleri

<400> 18  
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 Phe Ile Asn Tyr Tyr Asp Ser Glu Lys His Ala Glu Asn Ala Val Ile  
 35 40 45  
 Phe Leu His Gly Asn Ala Ala Ser Ser Tyr Leu Trp Arg His Val Val  
 50 55 60  
 Pro His Val Glu Pro Val Ala Arg Cys Ile Ile Pro Asp Leu Ile Gly  
 65 70 75 80  
 Met Gly Lys Ser Gly Lys Ser Gly Asn Gly Ser Tyr Arg Leu Leu Asp  
 85 90 95  
 His Tyr Lys Tyr Leu Thr Glu Trp Phe Lys His Leu Asn Leu Pro Lys  
 100 105 110  
 Lys Ile Ile Phe Val Gly His Asp Trp Gly Ala Cys Leu Ala Phe His  
 115 120 125  
 Tyr Cys Tyr Glu His Gln Asp Arg Ile Lys Ala Val His Ala Glu  
 130 135 140  
 Ser Val Val Asp Val Ile Glu Ser Trp Asp Glu Trp Pro Asp Ile Glu  
 145 150 155 160  
 Glu Asp Ile Ala Leu Ile Lys Ser Glu Gly Glu Lys Met Val Leu  
 165 170 175  
 Glu Asn Asn Phe Phe Val Glu Thr Met Leu Pro Ser Lys Ile Met Arg  
 180 185 190  
 Lys Leu Glu Pro Glu Glu Phe Ala Ala Tyr Leu Glu Pro Phe Lys Glu  
 195 200 205  
 Lys Gly Glu Val Arg Arg Pro Thr Leu Ser Trp Pro Arg Glu Ile Pro  
 210 215 220  
 Leu Val Lys Gly Gly Lys Pro Asp Val Val Glu Ile Val Arg Asn Tyr  
 225 230 235 240  
 Asn Ala Tyr Leu Arg Ala Ser His Asp Leu Pro Lys Met Phe Ile Glu  
 245 250 255  
 Ser Asp Pro Gly Phe Phe Ser Asn Ala Ile Val Glu Gly Ala Lys Lys  
 260 265 270  
 Phe Pro Asn Thr Glu Phe Val Lys Val Lys Gly Leu His Phe Ser Gln  
 275 280 285  
 Glu Asp Ala Pro Asp Glu Met Gly Asn Tyr Ile Lys Ser Phe Val Glu  
 290 295 300  
 Arg Val Leu Lys Asn Glu Gln  
 305 310

<210> 19  
 <211> 765  
 <212> DNA  
 <213> Gaussia

<220>  
 <221> CDS  
 <222> (37)...(594)

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 Met Gly Val Lys Val Leu  
 1 5

ttt gcc ctt att tgt att gct gtg gcc gag gcc aaa cca act gaa aac 102  
 Phe Ala Leu Ile Cys Ile Ala Val Ala Glu Ala Lys Pro Thr Glu Asn

10	15	20	
aat gaa gat ttc aac att gta gct gta gct agc aac ttt gct aca acg			150
Asn Glu Asp Phe Asn Ile Val Ala Val Ala Ser Asn Phe Ala Thr Thr			
25	30	35	
gat ctg gat gct gac cgt ggt aaa ttg ccc gga aaa aaa tta cca ctt			198
Asp Leu Asp Ala Asp Arg Gly Lys Leu Pro Gly Lys Lys Leu Pro Leu			
40	45	50	
gag gta ctg aaa gaa atg gaa gcc aat gct agg aaa gct ggc tgc act			246
Glu Val Leu Lys Glu Met Glu Ala Asn Ala Arg Lys Ala Gly Cys Thr			
55	60	65	70
agg gga tgt ctg ata tgc ctg tca cac atc aag tgt aca ccc aaa atg			294
Arg Gly Cys Leu Ile Cys Leu Ser His Ile Lys Cys Thr Pro Lys Met			
75	80	85	
aag aag ttt atc cca gga aga tgc cac acc tat gaa gga gac aaa gaa			342
Lys Lys Phe Ile Pro Gly Arg Cys His Thr Tyr Glu Gly Asp Lys Glu			
90	95	100	
agt gca cag gga gga ata gga gag gct att gtt gac att cct gaa att			390
Ser Ala Gln Gly Gly Ile Gly Glu Ala Ile Val Asp Ile Pro Glu Ile			
105	110	115	
cct ggg ttt aag gat ttg gaa ccc atg gaa caa ttc att gca caa gtt			438
Pro Gly Phe Lys Asp Leu Glu Pro Met Glu Gln Phe Ile Ala Gln Val			
120	125	130	
gac cta tgt gta gac tgc aca act gga tgc ctc aaa ggt ctt gcc aat			486
Asp Leu Cys Val Asp Cys Thr Thr Gly Cys Leu Lys Gly Leu Ala Asn			
135	140	145	150
gtg caa tgt tct gat tta ctg aag aaa tgg ctg cca caa aga tgt gca			534
Val Gln Cys Ser Asp Leu Leu Lys Lys Trp Leu Pro Gln Arg Cys Ala			
155	160	165	
act ttt gct agc aaa att caa ggc caa gtg gac aaa ata aag ggt gcc			582
Thr Phe Ala Ser Lys Ile Gln Gly Gln Val Asp Lys Ile Lys Gly Ala			
170	175	180	
ggg ggt gat taa tcctaataaga atactgcata actggatgat gatatactag			634
Gly Gly Asp *			
185			
cttattgctc ataaaaatggc catttttttgt aacaaatcga gtctatgtaa ttcaaaatc			694
ctaattaatt gttaatacat atgtaattcc tataaatata atttatgcaa tccaaaaaaa			754
aaaaaaaaa a			765

<210> 20  
 <211> 185  
 <212> PRT  
 <213> Renilla mulleri

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 1 5 10 15  
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 Ser Asn Phe Ala Thr Thr Asp Leu Asp Ala Asp Arg Gly Lys Leu Pro  
 35 40 45  
 Gly Lys Lys Leu Pro Leu Glu Val Leu Lys Glu Met Glu Ala Asn Ala  
 50 55 60  
 Arg Lys Ala Gly Cys Thr Arg Gly Cys Leu Ile Cys Leu Ser His Ile



65	Lys	Cys	Thr	Pro	Lys	Met	Lys	Lys	Phe	Ile	Pro	Gly	Arg	Cys	His	Thr
					85					90					95	
Tyr	Glu	Gly	Asp	Lys	Glu	Ser	Ala	Gln	Gly	Gly	Ile	Gly	Glu	Ala	Ile	
			100					105						110		
Val	Asp	Ile	Pro	Glu	Ile	Pro	Gly	Phe	Lys	Asp	Leu	Glu	Pro	Met	Glu	
		115					120					125				
Gln	Phe	Ile	Ala	Gln	Val	Asp	Leu	Cys	Val	Asp	Cys	Thr	Thr	Gly	Cys	
		130					135				140					
Leu	Lys	Gly	Leu	Ala	Asn	Val	Gln	Cys	Ser	Asp	Leu	Leu	Lys	Lys	Trp	
					150					155					160	
Leu	Pro	Gln	Arg	Cys	Ala	Thr	Phe	Ala	Ser	Lys	Ile	Gln	Gly	Gln	Val	
			165						170					175		
Asp	Lys	Ile	Lys	Gly	Ala	Gly	Gly	Asp								
			180					185								

<210> 21  
 <211> 1146  
 <212> DNA  
 <213> Gaussia

<220>  
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 <222> (1)...(1146)  
 <223> Nucleotide sequence encoding a CBD-Gaussia  
 luciferase fusion protein

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1 5 10 15	
att aca cca ata atc aaa att act aac aca tct gac agt gat tta aat	96
Ile Thr Pro Ile Ile Lys Ile Thr Asn Thr Ser Asp Ser Asp Leu Asn	
20 25 30	
tta aat gac gta aaa gtt aga tat tat tac aca agt gat ggt aca caa	144
Leu Asn Asp Val Lys Val Arg Tyr Tyr Tyr Thr Ser Asp Gly Thr Gln	
35 40 45	
gga caa act ttc tgg tgt gac cat gct ggt gca tta tta gga aat agc	192
Gly Gln Thr Phe Trp Cys Asp His Ala Gly Ala Leu Leu Gly Asn Ser	
50 55 60	
tat gtt gat aac act agc aaa gtg aca gca aac ttc gtt aaa gaa aca	240
Tyr Val Asp Asn Thr Ser Lys Val Thr Ala Asn Phe Val Lys Glu Thr	
65 70 75 80	
gca agc cca aca tca acc tat gat aca tat gtt gaa ttt gga ttt gca	288
Ala Ser Pro Thr Ser Thr Tyr Asp Thr Tyr Val Glu Phe Gly Phe Ala	
85 90 95	
agc gga gca gct act ctt aaa aaa gga caa ttt ata act att caa gga	336
Ser Gly Ala Ala Thr Leu Lys Lys Gly Gln Phe Ile Thr Ile Gln Gly	
100 105 110	
aga ata aca aaa tca gac tgg tca aac tac act caa aca aat gac tat	384
Arg Ile Thr Lys Ser Asp Trp Ser Asn Tyr Thr Gln Thr Asn Asp Tyr	
115 120 125	
tca ttt gat gca agt agt tca aca cca gtt gta aat cca aaa gtt aca	432
Ser Phe Asp Ala Ser Ser Ser Thr Pro Val Val Asn Pro Lys Val Thr	
130 135 140	
gga tat ata ggt gga gct aaa gtt ctt ggt aca gca cca ggt tcc gcg	480

Gly 145	Tyr	Ile	Gly	Gly	Ala 150	Lys	Val	Leu	Gly	Thr 155	Ala	Pro	Gly	Ser	Ala 160	
ggt	ctg	gtg	cca	cgc	ggt	agt	act	gca	att	ggt	atg	aaa	gaa	acc	gct	528
Gly	Leu	Val	Pro	Arg 165	Gly	Ser	Thr	Ala	Ile 170	Gly	Met	Lys	Glu	Thr 175	Ala	
gct	gct	aaa	ttc	gaa	cgc	cag	cac	atg	gac	agc	cca	gat	ctg	ggt	acc	576
Ala	Ala	Lys	Phe 180	Glu	Arg	Gln	His	Met 185	Asp	Ser	Pro	Asp	Leu 190	Gly	Thr	
gat	gac	gac	gac	aag	atg	gga	gtg	aaa	ggt	ctt	ttt	gcc	ctt	att	tgt	624
Asp	Asp	Asp	Asp 195	Lys	Met	Gly	Val 200	Lys	Val	Leu	Phe	Ala 205	Leu	Ile	Cys	
att	gct	gtg	gcc	gag	gcc	aaa	cca	act	gaa	aac	aat	gaa	gat	ttc	aac	672
Ile	Ala	Val	Ala	Glu	Ala	Lys 215	Pro	Thr	Glu	Asn	Asn 220	Glu	Asp	Phe	Asn	
att	gta	gct	gta	gct	agc	aac	ttt	gct	aca	acg	gat	ctc	gat	gct	gac	720
Ile	Val	Ala	Val	Ala	Ser 230	Asn	Phe	Ala	Thr	Thr 235	Asp	Leu	Asp	Ala	Asp 240	
cgt	ggt	aaa	ttg	ccc	gga	aaa	aaa	tta	cca	ctt	gag	gta	ctc	aaa	gaa	768
Arg	Gly	Lys	Leu	Pro 245	Gly	Lys	Lys	Leu	Pro 250	Leu	Glu	Val	Leu	Lys 255	Glu	
atg	gaa	gcc	aat	gct	agg	aaa	gct	ggc	tgc	act	agg	gga	tgt	ctg	ata	816
Met	Glu	Ala	Asn 260	Ala	Arg	Lys	Ala	Gly 265	Cys	Thr	Arg	Gly	Cys 270	Leu	Ile	
tgc	ctg	tca	cac	atc	aag	tgt	aca	ccc	aaa	atg	aag	aag	ttt	atc	cca	864
Cys	Leu	Ser 275	His	Ile	Lys	Cys	Thr 280	Pro	Lys	Met	Lys	Lys 285	Phe	Ile	Pro	
gga	aga	tgc	cac	acc	tat	gaa	gga	gac	aaa	gaa	agt	gca	cag	gga	gga	912
Gly	Arg 290	Cys	His	Thr	Tyr	Glu 295	Gly	Asp	Lys	Glu	Ser 300	Ala	Gln	Gly	Gly	
ata	gga	gag	gct	att	gtt	gac	att	cct	gaa	att	cct	ggg	ttt	aag	gat	960
Ile	Gly	Glu	Ala	Ile	Val 310	Asp	Ile	Pro	Glu	Ile 315	Pro	Gly	Phe	Lys	Asp 320	
ttg	gaa	ccc	atg	gaa	caa	ttc	att	gca	caa	gtt	gac	cta	tgt	gta	gac	1008
Leu	Glu	Pro	Met	Glu 325	Gln	Phe	Ile	Ala	Gln 330	Val	Asp	Leu	Cys	Val 335	Asp	
tgc	aca	act	gga	tgc	ctc	aaa	ggt	ctt	gcc	aat	gtg	caa	tgt	tct	gat	1056
Cys	Thr	Thr	Gly 340	Cys	Leu	Lys	Gly	Leu 345	Ala	Asn	Val	Gln	Cys 350	Ser	Asp	
tta	ctc	aag	aaa	tgg	ctg	cca	caa	aga	tgt	gca	act	ttt	gct	agc	aaa	1104
Leu	Leu	Lys 355	Lys	Trp	Leu	Pro	Gln 360	Arg	Cys	Ala	Thr	Phe 365	Ala	Ser	Lys	
att	caa	ggc	caa	gtg	gac	aaa	ata	aag	ggt	gcc	ggt	ggt	gat			1146
Ile	Gln	Gly	Gln	Val	Asp 370	Lys 375	Ile	Lys	Gly	Ala	Gly 380	Gly	Asp			

<210> 22  
 <211> 382  
 <212> PRT  
 <213> Gaussia

&lt;400&gt; 22

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Ile Thr Pro Ile Lys Ile Thr Asn Thr Ser Asp Ser Asp Leu Asn
 20      25      30
Leu Asn Asp Val Lys Val Arg Tyr Tyr Tyr Thr Ser Asp Gly Thr Gln
 35      40      45
Gly Gln Thr Phe Trp Cys Asp His Ala Gly Ala Leu Leu Gly Asn Ser
 50      55      60
Tyr Val Asp Asn Thr Ser Lys Val Thr Ala Asn Phe Val Lys Glu Thr
 65      70      75      80
Ala Ser Pro Thr Ser Thr Tyr Asp Thr Tyr Val Glu Phe Gly Phe Ala
 85      90      95
Ser Gly Ala Ala Thr Leu Lys Lys Gly Gln Phe Ile Thr Ile Gln Gly
100     105     110
Arg Ile Thr Lys Ser Asp Trp Ser Asn Tyr Thr Gln Thr Asn Asp Tyr
115     120     125
Ser Phe Asp Ala Ser Ser Ser Thr Pro Val Val Asn Pro Lys Val Thr
130     135     140
Gly Tyr Ile Gly Gly Ala Lys Val Leu Gly Thr Ala Pro Gly Ser Ala
145     150     155     160
Gly Leu Val Pro Arg Gly Ser Thr Ala Ile Gly Met Lys Glu Thr Ala
165     170     175
Ala Ala Lys Phe Glu Arg Gln His Met Asp Ser Pro Asp Leu Gly Thr
180     185     190
Asp Asp Asp Asp Lys Met Gly Val Lys Val Leu Phe Ala Leu Ile Cys
195     200     205
Ile Ala Val Ala Glu Ala Lys Pro Thr Glu Asn Asn Glu Asp Phe Asn
210     215     220
Ile Val Ala Val Ala Ser Asn Phe Ala Thr Thr Asp Leu Asp Ala Asp
225     230     235     240
Arg Gly Lys Leu Pro Gly Lys Lys Leu Pro Leu Glu Val Leu Lys Glu
245     250     255
Met Glu Ala Asn Ala Arg Lys Ala Gly Cys Thr Arg Gly Cys Leu Ile
260     265     270
Cys Leu Ser His Ile Lys Cys Thr Pro Lys Met Lys Lys Phe Ile Pro
275     280     285
Gly Arg Cys His Thr Tyr Glu Gly Asp Lys Glu Ser Ala Gln Gly Gly
290     295     300
Ile Gly Glu Ala Ile Val Asp Ile Pro Glu Ile Pro Gly Phe Lys Asp
305     310     315     320
Leu Glu Pro Met Glu Gln Phe Ile Ala Gln Val Asp Leu Cys Val Asp
325     330     335
Cys Thr Thr Gly Cys Leu Lys Gly Leu Ala Asn Val Gln Cys Ser Asp
340     345     350
Leu Leu Lys Lys Trp Leu Pro Gln Arg Cys Ala Thr Phe Ala Ser Lys
355     360     365
Ile Gln Gly Gln Val Asp Lys Ile Lys Gly Ala Gly Gly Asp
370     375     380

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&lt;210&gt; 23

&lt;211&gt; 864

&lt;212&gt; DNA

&lt;213&gt; Renilla reniformis

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (61)...(762)

&lt;223&gt; GFP Clone-1

&lt;400&gt; 23

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ggcagcagggg tttcctgaca caataaaaac ctttcaaatt gtttctctgt agcagtaagt      60
atg gat ctc gca aaa ctt ggt ttg aag gaa gtg atg cct act aaa atc      108
Met Asp Leu Ala Lys Leu Gly Leu Lys Glu Val Met Pro Thr Lys Ile
 1      5      10      15

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aac tta gaa gga ctg gtt ggc gac cac gct ttc tca atg gaa gga gtt 156  
 Asn Leu Glu Gly Leu Val Gly Asp His Ala Phe Ser Met Glu Gly Val  
                   20                  25                  30

ggc gaa ggc aac ata ttg gaa gga act caa gag gtg aag ata tcg gta 204  
 Gly Glu Gly Asn Ile Leu Glu Gly Thr Gln Glu Val Lys Ile Ser Val  
                   35                  40                  45

aca aaa ggc gca cca ctc cca ttc gca ttt gat atc gta tct gtg gct 252  
 Thr Lys Gly Ala Pro Leu Pro Phe Ala Phe Asp Ile Val Ser Val Ala  
                   50                  55                  60

ttt tca tat ggg aac aga gct tat acc ggt tac cca gaa gaa att tcc 300  
 Phe Ser Tyr Gly Asn Arg Ala Tyr Thr Gly Tyr Pro Glu Glu Ile Ser  
                   65                  70                  75                  80

gac tac ttc ctc cag tcg ttt cca gaa ggc ttt act tac gag aga aac 348  
 Asp Tyr Phe Leu Gln Ser Phe Pro Glu Gly Phe Thr Tyr Glu Arg Asn  
                   85                  90                  95

att cgt tat caa gat gga gga act gca att gtt aaa tct gat ata agc 396  
 Ile Arg Tyr Gln Asp Gly Gly Thr Ala Ile Val Lys Ser Asp Ile Ser  
                   100                  105                  110

ttg gaa gat ggt aaa ttc ata gtg aat gta gac ttc aaa gcg aag gat 444  
 Leu Glu Asp Gly Lys Phe Ile Val Asn Val Asp Phe Lys Ala Lys Asp  
                   115                  120                  125

cta cgt cgc atg gga cca gtc atg cag caa gac atc gtg ggt atg cag 492  
 Leu Arg Arg Met Gly Pro Val Met Gln Gln Asp Ile Val Gly Met Gln  
                   130                  135                  140

cca tcg tat gag tca atg tac acc aat gtc act tca gtt ata ggg gaa 540  
 Pro Ser Tyr Glu Ser Met Tyr Thr Asn Val Thr Ser Val Ile Gly Glu  
                   145                  150                  155                  160

tgt ata ata gca ttc aaa ctt caa act ggc aag cat ttc act tac cac 588  
 Cys Ile Ile Ala Phe Lys Leu Gln Thr Gly Lys His Phe Thr Tyr His  
                   165                  170                  175

atg agg aca gtt tac aaa tca aag aag cca gtg gaa act atg cca ttg 636  
 Met Arg Thr Val Tyr Lys Ser Lys Lys Pro Val Glu Thr Met Pro Leu  
                   180                  185                  190

tat cat ttc atc cag cat cgc ctc gtt aag acc aat gtg gac aca gcc 684  
 Tyr His Phe Ile Gln His Arg Leu Val Lys Thr Asn Val Asp Thr Ala  
                   195                  200                  205

agt ggt tac gtt gtg caa cac gag aca gca att gca gcg cat tct aca 732  
 Ser Gly Tyr Val Val Gln His Glu Thr Ala Ile Ala Ala His Ser Thr  
                   210                  215                  220

atc aaa aaa att gaa ggc tct tta cca tag atacctgtac acaattattc 782  
 Ile Lys Lys Ile Glu Gly Ser Leu Pro \*  
 225                  230

tatgcacgta gcattttttt ggaaatataa gtggtattgt tcaataaaaat attaaatata 842  
 aaaaaaaaaa aaaaaaaaaa aa 864

&lt;210&gt; 24

&lt;211&gt; 860

&lt;212&gt; DNA

&lt;213&gt; Renilla reniformis

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (57)...(758)

&lt;223&gt; GFP Clone-2

&lt;400&gt; 24

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                                     Met
                                     1

gat ctc gca aaa ctt ggt ttg aag gaa gtg atg cct act aaa atc aac      107
Asp Leu Ala Lys Leu Gly Leu Lys Glu Val Met Pro Thr Lys Ile Asn
                    5                      10                      15

tta gaa gga ctg gtt ggc gac cac gct ttc tca atg gaa gga gtt ggc      155
Leu Glu Gly Leu Val Gly Asp His Ala Phe Ser Met Glu Gly Val Gly
                    20                      25                      30

gaa ggc aac ata ttg gaa gga act caa gag gtg aag ata tcg gta aca      203
Glu Gly Asn Ile Leu Glu Gly Thr Gln Glu Val Lys Ile Ser Val Thr
                    35                      40                      45

aaa ggc gca cca ctc cca ttc gca ttt gat atc gta tct gtt gct ttc      251
Lys Gly Ala Pro Leu Pro Phe Ala Phe Asp Ile Val Ser Val Ala Phe
                    50                      55                      60                      65

tca tat ggg aac aga gct tat act ggt tac cca gaa gaa att tcc gac      299
Ser Tyr Gly Asn Arg Ala Tyr Thr Gly Tyr Pro Glu Glu Ile Ser Asp
                    70                      75                      80

tac ttc ctc cag tcg ttt cca gaa ggc ttt act tac gag aga aac att      347
Tyr Phe Leu Gln Ser Phe Pro Glu Gly Phe Thr Tyr Glu Arg Asn Ile
                    85                      90                      95

cgt tat caa gat gga gga act gca att gtt aaa tct gat ata agc ttg      395
Arg Tyr Gln Asp Gly Gly Thr Ala Ile Val Lys Ser Asp Ile Ser Leu
                    100                      105                      110

gaa gat ggt aaa ttc ata gtg aat gta gac ttc aaa gcg aag gat cta      443
Glu Asp Gly Lys Phe Ile Val Asn Val Asp Phe Lys Ala Lys Asp Leu
                    115                      120                      125

cgt cgc atg gga cca gtc atg cag caa gac atc gtg ggt atg cag cca      491
Arg Arg Met Gly Pro Val Met Gln Gln Asp Ile Val Gly Met Gln Pro
                    130                      135                      140                      145

tcg tat gag tca atg tac acc aat gtc act tca gtt ata ggg gaa tgt      539
Ser Tyr Glu Ser Met Tyr Thr Asn Val Thr Ser Val Ile Gly Glu Cys
                    150                      155                      160

ata ata gca ttc aaa ctt caa act ggc aaa cat ttc act tac cac atg      587
Ile Ile Ala Phe Lys Leu Gln Thr Gly Lys His Phe Thr Tyr His Met
                    165                      170                      175

agg aca gtt tac aaa tca aag aag cca gtg gaa act atg cca ttg tat      635
Arg Thr Val Tyr Lys Ser Lys Lys Pro Val Glu Thr Met Pro Leu Tyr
                    180                      185                      190

cat ttc atc cag cat cgc ctc gtt aag acc aat gtg gac aca gcc agt      683
His Phe Ile Gln His Arg Leu Val Lys Thr Asn Val Asp Thr Ala Ser
                    195                      200                      205

ggt tac gtt gtg caa cac gag aca gca att gca gcg cat tct aca atc      731
Gly Tyr Val Val Gln His Glu Thr Ala Ile Ala Ala His Ser Thr Ile
                    210                      215                      220                      225

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aaa aaa att gaa ggc tct tta cca tag atatctatac acaattattc 778  
 Lys Lys Ile Glu Gly Ser Leu Pro \*  
 230

tatgcacgta gcattttttt ggaaatataa gtggtattgt tcaataaaat attaaatata 838  
 aaaaaaaaaa aaaaaaaaaa aa 860

<210> 25  
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 <212> DNA  
 <213> Renilla reniformis

<220>  
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 <222> (61)...(762)  
 <223> GFP Clone-3

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 atg gat ctc gca aaa ctt ggt ttg aag gaa gtg atg cct act aaa atc 108  
 Met Asp Leu Ala Lys Leu Gly Leu Lys Glu Val Met Pro Thr Lys Ile  
 1 5 10 15  
 aac tta gaa gga ctg gtt ggc gac cac gct ttc tca atg gaa gga gtt 156  
 Asn Leu Glu Gly Leu Val Gly Asp His Ala Phe Ser Met Glu Gly Val  
 20 25 30  
 ggc gaa ggc aac ata ttg gaa gga act caa gag gtg aag ata tcg gta 204  
 Gly Glu Gly Asn Ile Leu Glu Gly Thr Gln Glu Val Lys Ile Ser Val  
 35 40 45  
 aca aaa ggc gca cca ctc cca ttc gca ttt gat atc gta tct gtg gct 252  
 Thr Lys Gly Ala Pro Leu Pro Phe Ala Phe Asp Ile Val Ser Val Ala  
 50 55 60  
 ttt tca tat ggg aac aga gct tat acc ggt tac cca gaa gaa att tcc 300  
 Phe Ser Tyr Gly Asn Arg Ala Tyr Thr Gly Tyr Pro Glu Glu Ile Ser  
 65 70 75 80  
 gac tac ttc ctc cag tcg ttt cca gaa ggc ttt act tac gag aga aac 348  
 Asp Tyr Phe Leu Gln Ser Phe Pro Glu Gly Phe Thr Tyr Glu Arg Asn  
 85 90 95  
 att cgt tat caa gat gga gga act gca att gtt aaa tct gat ata agc 396  
 Ile Arg Tyr Gln Asp Gly Gly Thr Ala Ile Val Lys Ser Asp Ile Ser  
 100 105 110  
 ttg gaa gat ggt aaa ttc ata gtg aat gta gac ttc aaa gcg aag gat 444  
 Leu Glu Asp Gly Lys Phe Ile Val Asn Val Asp Phe Lys Ala Lys Asp  
 115 120 125  
 cta cgt cgc atg gga cca gtc atg cag caa gac atc gtg ggt atg cag 492  
 Leu Arg Arg Met Gly Pro Val Met Gln Gln Asp Ile Val Gly Met Gln  
 130 135 140  
 cca tcg tat gag tca atg tac acc aat gtc act tca gtt ata ggg gaa 540  
 Pro Ser Tyr Glu Ser Met Tyr Thr Asn Val Thr Ser Val Ile Gly Glu  
 145 150 155 160  
 tgt ata ata gca ttc aaa ctt caa act ggc aag cat ttc act tac cac 588  
 Cys Ile Ile Ala Phe Lys Leu Gln Thr Gly Lys His Phe Thr Tyr His  
 165 170 175

atg agg aca gtt tac aaa tca aag aag cca gtg gaa act atg cca ttg 636  
 Met Arg Thr Val Tyr Lys Ser Lys Lys Pro Val Glu Thr Met Pro Leu  
 180 185 190

tat cat ttc atc cag cat cgc ctc gtt aag acc aat gtg gac aca gcc 684  
 Tyr His Phe Ile Gln His Arg Leu Val Lys Thr Asn Val Asp Thr Ala  
 195 200 205

agt ggt tac gtt gtg caa cac gag aca gca att gca gcg cat tct aca 732  
 Ser Gly Tyr Val Val Gln His Glu Thr Ala Ile Ala Ala His Ser Thr  
 210 215 220

atc aaa aaa att gaa ggc tct tta cca tag atacctgtac acaattattc 782  
 Ile Lys Lys Ile Glu Gly Ser Leu Pro \*  
 225 230

tatgcacgta gcattttttt ggaaatataa gtgggtattgt tcaataaaaat attaaatata 842  
 tgcttttgca aaaaaaaaaa aaaaaaaaaa a 873

<210> 26  
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 <212> DNA  
 <213> Renilla reniformis

<220>  
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 <223> Human codon optimized Renilla reniformis GFP

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 atg gac ctg gcc aag ctg ggc ctg aag gag gtg atg ccc acc aag atc 108  
 Met Asp Leu Ala Lys Leu Gly Leu Lys Glu Val Met Pro Thr Lys Ile  
 1 5 10 15

aac ctg gag ggc ctg gtg ggc gac cac gcc ttc tcg atg gag ggc gtg 156  
 Asn Leu Glu Gly Leu Val Gly Asp His Ala Phe Ser Met Glu Gly Val  
 20 25 30

ggc gag ggc aac atc ttg gag ggc acc cag gag gtg aag atc agc gtg 204  
 Gly Glu Gly Asn Ile Leu Glu Gly Thr Gln Glu Val Lys Ile Ser Val  
 35 40 45

acc aag ggc gcc ccc ctg ccc ttc gcc ttc gac atc gtg agc gtg gcc 252  
 Thr Lys Gly Ala Pro Leu Pro Phe Ala Phe Asp Ile Val Ser Val Ala  
 50 55 60

ttc agc tac ggc aac cgg gcc tac acc ggc tac ccc gag gag atc agc 300  
 Phe Ser Tyr Gly Asn Arg Ala Tyr Thr Gly Tyr Pro Glu Glu Ile Ser  
 65 70 75 80

gac tac ttc ctg cag agc ttc ccc gag ggc ttc acc tac gag cgg aac 348  
 Asp Tyr Phe Leu Gln Ser Phe Pro Glu Gly Phe Thr Tyr Glu Arg Asn  
 85 90 95

atc cgg tac cag gac ggc ggc acc gcc atc gtg aag agc gac atc agc 396  
 Ile Arg Tyr Gln Asp Gly Gly Thr Ala Ile Val Lys Ser Asp Ile Ser  
 100 105 110

ctg gag gac ggc aag ttc atc gtg aac gtg gac ttc aag gcc aag gac 444  
 Leu Glu Asp Gly Lys Phe Ile Val Asn Val Asp Phe Lys Ala Lys Asp  
 115 120 125

ctg cgg cgg atg ggc ccc gtg atg cag cag gac atc gtg ggc atg cag 492

Leu Arg Arg Met Gly Pro Val Met Gln Gln Asp Ile Val Gly Met Gln  
130 135 140

ccc agc tac gag agc atg tac acc aac gtg acc agc gtg atc ggc gag 540  
Pro Ser Tyr Glu Ser Met Tyr Thr Asn Val Thr Ser Val Ile Gly Glu  
145 150 155 160

tgc atc atc gcc ttc aag ctg cag acc ggc aag cac ttc acc tac cac 588  
Cys Ile Ile Ala Phe Lys Leu Gln Thr Gly Lys His Phe Thr Tyr His  
165 170 175

atg cgg acc gtg tac aag agc aag aag ccc gtg gag acc atg ccc ctg 636  
Met Arg Thr Val Tyr Lys Ser Lys Lys Pro Val Glu Thr Met Pro Leu  
180 185 190

tac cac ttc atc cag cac cgg ctg gtg aag acc aac gtg gac acc gcc 684  
Tyr His Phe Ile Gln His Arg Lys Val Lys Thr Asn Val Asp Thr Ala  
195 200 205

agc ggc tac gtg gtg cag cac gag aca gcc atc gcc gcc cac agc acc 732  
Ser Gly Tyr Val Val Gln His Glu Thr Ala Ile Ala Ala His Ser Thr  
210 215 220

atc aag aag atc gag ggc agc ctg ccc tagatacctg tacacaatta 779  
Ile Lys Lys Ile Glu Gly Ser Leu Pro  
225 230

ttctatgcac gtagcatttt ttgggaaata taagtgggtat tgttcaataa aatattaaat 839  
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<210> 27

<211> 233

<212> PRT

<213> Renilla reniformis

<400> 27

Met Asp Leu Ala Lys Leu Gly Leu Lys Glu Val Met Pro Thr Lys Ile  
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Asn Leu Glu Gly Leu Val Gly Asp His Ala Phe Ser Met Glu Gly Val  
20 25 30

Gly Glu Gly Asn Ile Leu Glu Gly Thr Gln Glu Val Lys Ile Ser Val  
35 40 45

Thr Lys Gly Ala Pro Leu Pro Phe Ala Phe Asp Ile Val Ser Val Ala  
50 55 60

Phe Ser Tyr Gly Asn Arg Ala Tyr Thr Gly Tyr Pro Glu Glu Ile Ser  
65 70 75 80

Asp Tyr Phe Leu Gln Ser Phe Pro Glu Gly Phe Thr Tyr Glu Arg Asn  
85 90 95

Ile Arg Tyr Gln Asp Gly Gly Thr Ala Ile Val Lys Ser Asp Ile Ser  
100 105 110

Leu Glu Asp Gly Lys Phe Ile Val Asn Val Asp Phe Lys Ala Lys Asp  
115 120 125

Leu Arg Arg Met Gly Pro Val Met Gln Gln Asp Ile Val Gly Met Gln  
130 135 140

Pro Ser Tyr Glu Ser Met Tyr Thr Asn Val Thr Ser Val Ile Gly Glu  
145 150 155 160

Cys Ile Ile Ala Phe Lys Leu Gln Thr Gly Lys His Phe Thr Tyr His  
165 170 175

Met Arg Thr Val Tyr Lys Ser Lys Lys Pro Val Glu Thr Met Pro Leu  
180 185 190

Tyr His Phe Ile Gln His Arg Leu Val Lys Thr Asn Val Asp Thr Ala  
195 200 205

Ser Gly Tyr Val Val Gln His Glu Thr Ala Ile Ala Ala His Ser Thr  
210 215 220

Ile Lys Lys Ile Glu Gly Ser Leu Pro



225

230

<210> 28  
 <211> 861  
 <212> DNA  
 <213> Pleuromamma

<220>  
 <221> CDS  
 <222> (148)...(741)  
 <223> Pleuormamma luciferase

<400> 28  
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 tcgctgaaag gtgatttctg tagtgatgtt tccttctggg atgtgatcaa gtacaacact 120  
 gagagtcgac aatgctgtga cacaaaa atg ctt aga aat tgc gct agg aag caa 174  
 Met Leu Arg Asn Cys Ala Arg Lys Gln  
 1 5

gag caa gtt tgc gcc gat gtg acc gag atg aaa tgc caa gca gtt gct 222  
 Glu Gln Val Cys Ala Asp Val Thr Glu Met Lys Cys Gln Ala Val Ala 25  
 10 15 20

tgg gcc gac tgt gga ccc aga ttt gat tcc act ggc agg aat aga tgc 270  
 Trp Ala Asp Cys Gly Pro Arg Phe Asp Ser Thr Gly Arg Asn Arg Cys 40  
 30 35

caa gtt caa tac aag gac tac gcg tac aag tcc tgc gtg gaa gtt gat 318  
 Gln Val Gln Tyr Lys Asp Tyr Ala Tyr Lys Ser Cys Val Glu Val Asp 55  
 45 50

tac act gta ccg cac agg aag caa gtt cca gag tgc aaa caa gtc act 366  
 Tyr Thr Val Pro His Arg Lys Gln Val Pro Glu Cys Lys Gln Val Thr 70  
 60 65

aaa gat aac tgc gtt act gat tgg gaa gtt gac gcc aat ggc aac aag 414  
 Lys Asp Asn Cys Val Thr Asp Trp Glu Val Asp Ala Asn Gly Asn Lys 85  
 75 80

gtt tgg ggt ggt acc gag aaa tgc act cct gtc act tgg gaa gaa tgt 462  
 Val Trp Gly Gly Thr Glu Lys Cys Thr Pro Val Thr Trp Glu Glu Cys 105  
 90 95 100

aat atc gtg gag aaa gat gta gat ttt cca act gtc aag acg gaa tgc 510  
 Asn Ile Val Glu Lys Asp Val Asp Phe Pro Thr Val Lys Thr Glu Cys 120  
 110 115

ggc atc ctg tct cac ctt aag tat gca gac ttc ata gag gga cct tcc 558  
 Gly Ile Leu Ser His Leu Lys Tyr Ala Asp Phe Ile Glu Gly Pro Ser 135  
 125 130

cac tct ttg tct atg aga acc aat tgt cag gtc aag agt tca ttg gac 606  
 His Ser Leu Ser Met Arg Thr Asn Cys Gln Val Lys Ser Ser Leu Asp 150  
 140 145

tgc cgg cct gtt aag acc agg aag tgt gca acg gtc gag tac cac gaa 654  
 Cys Arg Pro Val Lys Thr Arg Lys Cys Ala Thr Val Glu Tyr His Glu 165  
 155 160

tgc agc atg aag ccc caa gaa gac tgc agc cca gtc act gtt cat att 702  
 Cys Ser Met Lys Pro Gln Glu Asp Cys Ser Pro Val Thr Val His Ile 185  
 170 175 180

cct gac cag gag aaa gtt cac cag aag aag tgc ctc aca taaatgttat 751

Pro Asp Gln Glu Lys Val His Gln Lys Lys Cys Leu Thr  
 190 195

caatttttagc tcttactaat ttaaacataa taaatatcac atcgaagccc tttattttat 811  
 agaagtgtaa tgcttgaata aatctagtga ataaaaaaaa aaaaaaaaaa 861

<210> 29  
 <211> 198  
 <212> PRT  
 <213> Pleuromamma

<400> 29  
 Met Leu Arg Asn Cys Ala Arg Lys Gln Glu Gln Val Cys Ala Asp Val  
 1 5 10 15  
 Thr Glu Met Lys Cys Gln Ala Val Ala Trp Ala Asp Cys Gly Pro Arg  
 20 25 30  
 Phe Asp Ser Thr Gly Arg Asn Arg Cys Gln Val Gln Tyr Lys Asp Tyr  
 35 40 45  
 Ala Tyr Lys Ser Cys Val Glu Val Asp Tyr Thr Val Pro His Arg Lys  
 50 55 60  
 Gln Val Pro Glu Cys Lys Gln Val Thr Lys Asp Asn Cys Val Thr Asp  
 65 70 75 80  
 Trp Glu Val Asp Ala Asn Gly Asn Lys Val Trp Gly Gly Thr Glu Lys  
 85 90 95  
 Cys Thr Pro Val Thr Trp Glu Glu Cys Asn Ile Val Glu Lys Asp Val  
 100 105 110  
 Asp Phe Pro Thr Val Lys Thr Glu Cys Gly Ile Leu Ser His Leu Lys  
 115 120 125  
 Tyr Ala Asp Phe Ile Glu Gly Pro Ser His Ser Leu Ser Met Arg Thr  
 130 135 140  
 Asn Cys Gln Val Lys Ser Ser Leu Asp Cys Arg Pro Val Lys Thr Arg  
 145 150 155 160  
 Lys Cys Ala Thr Val Glu Tyr His Glu Cys Ser Met Lys Pro Gln Glu  
 165 170 175  
 Asp Cys Ser Pro Val Thr Val His Ile Pro Asp Gln Glu Lys Val His  
 180 185 190  
 Gln Lys Lys Cys Leu Thr  
 195

<210> 30  
 <211> 1104  
 <212> DNA  
 <213> Ptilosarcus gurneyi

<220>  
 <221> CDS  
 <222> (34)...(747)  
 <223> Ptilosarcus Green Fluorescent Protein

<400> 30  
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 Met Asn Arg Asn Val Leu Lys  
 1 5  
 aac act gga ctg aaa gag att atg tcg gca aaa gct agc gtt gaa gga 102  
 Asn Thr Gly Leu Lys Glu Ile Met Ser Ala Lys Ala Ser Val Glu Gly  
 10 15 20  
 atc gtg aac aat cac gtt ttt tcc atg gaa gga ttt gga aaa ggc aat 150  
 Ile Val Asn Asn His Val Phe Ser Met Glu Gly Phe Gly Lys Gly Asn  
 25 30 35  
 gta tta ttt gga aac caa ttg atg caa atc cgg gtt aca aag gga ggt 198  
 Val Leu Phe Gly Asn Gln Leu Met Gln Ile Arg Val Thr Lys Gly Gly  
 40 45 50 55

ccg ttg cca ttc gct ttc gat att gtt tcc ata gct ttc caa tac ggg 246  
 Pro Leu Pro Phe Ala Phe Asp Ile Val Ser Ile Ala Phe Gln Tyr Gly  
 60 65 70  
 aat cgc act ttc acg aaa tac cca gac gac att gcg gac tac ttt gtt 294  
 Asn Arg Thr Phe Thr Lys Tyr Pro Asp Asp Ile Ala Asp Tyr Phe Val  
 75 80 85  
 caa tca ttc ccg gct gga ttt ttc tac gaa aga aat cta cgc ttt gaa 342  
 Gln Ser Phe Pro Ala Gly Phe Phe Tyr Glu Arg Asn Leu Arg Phe Glu  
 90 95 100  
 gat ggc gcc att gtt gac att cgt tca gat ata agt tta gaa gat gat 390  
 Asp Gly Ala Ile Val Asp Ile Arg Ser Asp Ile Ser Leu Glu Asp Asp  
 105 110 115  
 aag ttc cac tac aaa gtg gag tat aga ggc aac ggt ttc cct agt aac 438  
 Lys Phe His Tyr Lys Val Glu Tyr Arg Gly Asn Gly Phe Pro Ser Asn  
 120 125 130 135  
 gga ccc gtg atg caa aaa gcc atc ctc ggc atg gag cca tcg ttt gag 486  
 Gly Pro Val Met Gln Lys Ala Ile Leu Gly Met Glu Pro Ser Phe Glu  
 140 145 150  
 gtg gtc tac atg aac agc ggc gtt ctg gtg ggc gaa gta gat ctc gtt 534  
 Val Val Tyr Met Asn Ser Gly Val Leu Val Gly Glu Val Asp Leu Val  
 155 160 165  
 tac aaa ctc gag tca ggg aac tat tac tcg tgc cac atg aaa acg ttt 582  
 Tyr Lys Leu Glu Ser Gly Asn Tyr Tyr Ser Cys His Met Lys Thr Phe  
 170 175 180  
 tac aga tcc aaa ggt gga gtg aaa gaa ttc ccg gaa tat cac ttt atc 630  
 Tyr Arg Ser Lys Gly Gly Val Lys Glu Phe Pro Glu Tyr His Phe Ile  
 185 190 195  
 cat cat cgt ctg gag aaa acc tac gtg gaa gaa gga agc ttc gtg gaa 678  
 His His Arg Leu Glu Lys Thr Tyr Val Glu Glu Gly Ser Phe Val Glu  
 200 205 210 215  
 caa cac gag acg gcc att gca caa ctg acc aca att gga aaa cct ctg 726  
 Gln His Glu Thr Ala Ile Ala Gln Leu Thr Thr Ile Gly Lys Pro Leu  
 220 225 230  
 ggc tcc ctt cat gaa tgg gtg tagaaaatga ccaatatact ggggaaaccg 777  
 Gly Ser Leu His Glu Trp Val  
 235  
 ataaccgttt ggaagcttgt gtatacaaat tatttggggt cattttgttaa tgtgtatgtg 837  
 tgttgtatga tcaatagacg tcgtcattca tagcttgaat ccttcagcaa aagaaacctc 897  
 gaagcatatt gaaacctcga agcatattga aacctcgacg gagagcgtaa agagaccgca 957  
 caaattaacg cgtttcaacc agcagttgga atctttaaac cgatcaaaac tattaatata 1017  
 aatatatata ccctgtataa cttatatata tctatatagt ttgatattga ttaaattctgt 1077  
 tcttgatcaa aaaaaaaaaa aaaaaaa 1104

<210> 31  
 <211> 1279  
 <212> DNA  
 <213> Ptilosarcus gurneyi

<220>  
 <221> CDS  
 <222> (7) ... (720)

## &lt;223&gt; Ptilosarcus Green Flourescent Protein (GFP)

&lt;400&gt; 31

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Met Asn Arg Asn Val Leu Lys Asn Thr Gly Leu Lys Glu Ile	
1 5 10	
atg tcg gca aaa gct agc gtt gaa gga atc gtg aac aat cac gtt ttt	96
Met Ser Ala Lys Ala Ser Val Glu Gly Ile Val Asn Asn His Val Phe	
15 20 25 30	
tcc atg gaa gga ttt gga aaa ggc aat gta tta ttt gga aac caa ttg	144
Ser Met Glu Gly Phe Gly Lys Gly Asn Val Leu Phe Gly Asn Gln Leu	
35 40 45	
atg caa atc cgg gtt aca aag gga ggt ccg ttg cca ttc gct ttc gac	192
Met Gln Ile Arg Val Thr Lys Gly Gly Pro Leu Pro Phe Ala Phe Asp	
50 55 60	
att gtt tcc ata gct ttc caa tac ggg aat cgc act ttc acg aaa tac	240
Ile Val Ser Ile Ala Phe Gln Tyr Gly Asn Arg Thr Phe Thr Lys Tyr	
65 70 75	
cca gac gac att gcg gac tac ttt gtt caa tca ttt ccg gct gga ttt	288
Pro Asp Asp Ile Ala Asp Tyr Phe Val Gln Ser Phe Pro Ala Gly Phe	
80 85 90	
ttc tac gaa aga aat cta cgc ttt gaa gat ggc gcc att gtt gac att	336
Phe Tyr Glu Arg Asn Leu Arg Phe Glu Asp Gly Ala Ile Val Asp Ile	
95 100 105 110	
cgt tca gat ata agt tta gaa gat gat aag ttc cac tac aaa gtg gag	384
Arg Ser Asp Ile Ser Leu Glu Asp Asp Lys Phe His Tyr Lys Val Glu	
115 120 125	
tat aga ggc aac ggt ttc cct agt aac gga ccc gtg atg caa aaa gcc	432
Tyr Arg Gly Asn Gly Phe Pro Ser Asn Gly Pro Val Met Gln Lys Ala	
130 135 140	
atc ctc ggc atg gag cca tcg ttt gag gtg gtc tac atg aac agc ggc	480
Ile Leu Gly Met Glu Pro Ser Phe Glu Val Val Tyr Met Asn Ser Gly	
145 150 155	
gtt ctg gtg ggc gaa gta gat ctc gtt tac aaa ctc gag tca ggg aac	528
Val Leu Val Gly Glu Val Asp Leu Val Tyr Lys Leu Glu Ser Gly Asn	
160 165 170	
tat tac tcg tgc cac atg aaa acg ttt tac aga tcc aaa ggt gga gtg	576
Tyr Tyr Ser Cys His Met Lys Thr Phe Tyr Arg Ser Lys Gly Gly Val	
175 180 185 190	
aaa gaa ttc ccg gaa tat cac ttt atc cat cat cgt ctg gag aaa acc	624
Lys Glu Phe Pro Glu Tyr His Phe Ile His Arg Leu Glu Lys Thr	
195 200 205	
tac gtg gaa gaa gga agc ttc gtg gaa caa cac gag acg gcc att gca	672
Tyr Val Glu Glu Gly Ser Phe Val Glu Gln His Glu Thr Ala Ile Ala	
210 215 220	
caa ctg acc aca att gga aaa cct ctg ggc tcc ctt cat gaa tgg gtg	720
Gln Leu Thr Thr Ile Gly Lys Pro Leu Gly Ser Leu His Glu Trp Val	
225 230 235	
tagaaaaatga ccaatataact ggggaaaatc accaatatac tggggaaaat gaccaattta	780
ctggggaaaaa tgaccaatat actgtagaaa atcaccaata tactggggaa aatgaccaat	840

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ttactgggga aatgaccaat ttactgtaga aaatcaccaa tatactgtgg aaaatgacca 900
aaatactgta gaaatgttca cactgggttg ataaccgttt cgataaccgt ttggaagctt 960
gtgtatacaa gttatttggg gtcattttgt aatgtgtatg tgtgttgtat gatctataga 1020
cgtcgtcatt catagcttga atccttcagc aaaagaaacc tcgaagcata ttgaaacctc 1080
gacggagagc ataaagagac cgcacgtaca caaattataa taccagcagt tggaatcttt 1140
aaaccgatca aaactattaa tatatatata caccctgtat aacatatata tatatatata 1200
tctacatagt ttgatattga ttaaactctgt tcttgatcac taaaaaaaaa aaaaaaaaaa 1260
aaaaaaaaaa aaaaaaaaaa 1279

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&lt;210&gt; 32

&lt;211&gt; 238

&lt;212&gt; PRT

&lt;213&gt; Ptilosarcus gurneyi

&lt;400&gt; 32

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Met Asn Arg Asn Val Leu Lys Asn Thr Gly Leu Lys Glu Ile Met Ser
1 5 10 15
Ala Lys Ala Ser Val Glu Gly Ile Val Asn Asn His Val Phe Ser Met
20 25 30
Glu Gly Phe Gly Lys Gly Asn Val Leu Phe Gly Asn Gln Leu Met Gln
35 40 45
Ile Arg Val Thr Lys Gly Gly Pro Leu Pro Phe Ala Phe Asp Ile Val
50 55 60
Ser Ile Ala Phe Gln Tyr Gly Asn Arg Thr Phe Thr Lys Tyr Pro Asp
65 70 75 80
Asp Ile Ala Asp Tyr Phe Val Gln Ser Phe Pro Ala Gly Phe Phe Tyr
85 90 95
Glu Arg Asn Leu Arg Phe Glu Asp Gly Ala Ile Val Asp Ile Arg Ser
100 105 110
Asp Ile Ser Leu Glu Asp Asp Lys Phe His Tyr Lys Val Glu Tyr Arg
115 120 125
Gly Asn Gly Phe Pro Ser Asn Gly Pro Val Met Gln Lys Ala Ile Leu
130 135 140
Gly Met Glu Pro Ser Phe Glu Val Val Tyr Met Asn Ser Gly Val Leu
145 150 155 160
Val Gly Glu Val Asp Leu Val Tyr Lys Leu Glu Ser Gly Asn Tyr Tyr
165 170 175
Ser Cys His Met Lys Thr Phe Tyr Arg Ser Lys Gly Gly Val Lys Glu
180 185 190
Phe Pro Glu Tyr His Phe Ile His Arg Leu Glu Lys Thr Tyr Val
195 200 205
Glu Glu Gly Ser Phe Val Glu Gln His Glu Thr Ala Ile Ala Gln Leu
210 215 220
Thr Thr Ile Gly Lys Pro Leu Gly Ser Leu His Glu Trp Val
225 230 235

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&lt;210&gt; 33

&lt;211&gt; 233

&lt;212&gt; PRT

&lt;213&gt; Renilla Reniformis mutein

&lt;400&gt; 33

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Met Asp Leu Ala Lys Leu Gly Leu Lys Glu Val Met Pro Thr Lys Ile
1 5 10 15
Asn Leu Glu Gly Leu Val Gly Asp His Ala Phe Ser Met Glu Gly Val
20 25 30
Gly Glu Gly Asn Ile Leu Glu Gly Thr Gln Glu Val Lys Ile Ser Val
35 40 45
Thr Lys Gly Ala Pro Leu Pro Phe Ala Phe Asp Ile Val Ser Val Ala
50 55 60
Phe Ser Tyr Gly Asn Arg Ala Tyr Thr Gly Tyr Pro Glu Glu Ile Ser
65 70 75 80
Asp Tyr Phe Leu Gln Ser Phe Pro Glu Gly Phe Thr Tyr Glu Arg Asn
85 90 95
Ile Arg Tyr Gln Asp Gly Gly Thr Ala Ile Val Asp Ser Asp Ile Ser

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	100		105		110
Leu Glu Asp	Gly Lys Phe Ile Val Asn Val Asp Phe Lys Ala Asp Asp				
115		120		125	
Leu Arg Asp	Met Gly Pro Val Met Gln Gln Asp Ile Val Gly Met Gln				
130		135		140	
Pro Ser Tyr Glu Ser Met Tyr Thr Asn Val Thr Ser Val Ile Gly Glu					
145		150		155	160
Cys Ile Ile Ala Phe Lys Leu Gln Thr Gly Lys Asp Phe Thr Tyr His					
	165	170		175	
Met Arg Thr Val Tyr Lys Ser Lys Lys Pro Val Glu Thr Met Pro Leu					
	180	185		190	
Tyr His Phe Ile Gln His Asp Leu Val Lys Thr Asn Val Asp Thr Ala					
195		200		205	
Ser Gly Tyr Val Val Gln His Glu Thr Ala Ile Ala Ala His Ser Thr					
210		215		220	
Ile Asp Lys Ile Glu Gly Ser Leu Pro					
225		230			